

1 CGCCCGCGGG CTGAGCTCG CGATCTGGC CCCAGCGAGG CGGTGGGCG
 51 GGGCGGGCG GGGCGGGCG CGCAGCAGGA CGCAGTGGG CCGCCCGCG
 101 GGCCACGGAC ACTGTCGCC CGCGCCCAGG TTCCAACAA GGCTACGCAG
 151 AAGAACCCCC TTGACTGAG CAATGGAGGG GGGTCCAGCT GTCTGCTGCC
 201 AGGATCCTCG GGCAGAGCTG TAGAACCGGG TGGCAGCCAT CGATGTGACT
 251 CACTTGGAGG AGGCAGATGG TGCCCAAGAG CCTACTAGAA ACGGTGTGGA
 301 CCCCCCACCA CGGGCCAGAG CTGCCTCTGT GATCCCTGGC AGTACTTCAA
 351 GACTGCTCCC AGCCCCGGCT AGCCTCTCAG CCAGGAAGCT TTCCCTACAG
 401 GAGCGGCCAG CAGGAAGCTA TCTGGAGGC CAGGCTGGC CTTATGCCAC
 451 GGGGCCTGCC AGCCACATCT CCCCCCGGGC CTGGCGGAGG CCCACCATCG
 501 AGTCCCACCA CGTGGCCATC TCAGATGCAG AGGACTGCGT GCAGCTGAAC
 551 CAGTACAAGC TGCAAGTGA GATTGGCAAG GGTGCCTACG GTGTGGTGAG
 601 GCTGGCCTAC AACGAAAGTG AAGACAGACA CTATGCAATG AAAGTCCTT
 651 CAAAAAAGAA GTTACTGAAG CAGTATGGCT TTCCACGTCG CCCTCCCCG
 701 AGAGGGTCCC AGGCTGCCA GGGAGGACCA GCCAAGCAGC TGCTGCCCT
 751 GGAGCGGGTG TACCAGGAGA TTGCATCCT GAAGAAGCTG GACCACGTGA
 801 ATGTGGTCAA ACTGATCGAG GTCCCTGGATG ACCCAGCTGA GGACAACCTC
 851 TATTTGGTGT TTGACCTCTT GAGAAAGGGG CCCGTCATGG AAGTGCCCTG
 901 TGACAAGCCC TTCTCGGAGG AGCAAGCTCG CCTCTACCTG CGGGACGTCA
 951 TCCCTGGGCT CGAGTAATTG CACTGCCAGA AGATCGTCA CAGGGACATC
 1001 AAGCCATCCA ACCTGCTCTT GGGGGATGAT GGGCACGTCG AGATGCCGA
 1051 CTTTGGCGTC AGCAACCACT TTGAGGGGAA CGACGCTCAG CTGTCAGCA
 1101 CGCGGGAAAC CCCAGCATTC ATGGCCCCCG AGGCCATTTC TGATTCGGC
 1151 CAGAGCTTCAG GTGGGAAGGC CTTGGATGTA TGGGCCACTG GCGTCACGTT
 1201 GTACTGCTTT GTCTATGGG AGTGCCATT CATCGACGAT TTCACTCTGG
 1251 CCCTCCACAG GAAGATCAAG AATGAGCCCC TGTTGTTTCC TGAGGAGCCA
 1301 GAAATCAGCG AGGAGCTCAA GGACCTGATC CTGAAGATGT TAGACAAGAA
 1351 TCCCGAGACG AGAATTGGGG TGCCAGACAT CAAGTTGAC CTTGGGTGA
 1401 CCAAGAACGG GGAGGAGGCC CTTCTTCGG AGGAGGAGCA CTGCAGCGTG
 1451 GTGGAGGTGA CAGAGGGGA GGTAAAGAAC TCAGTCAGGC TCATCCCCAG
 1501 CTGGACCACCG GTGATCCTGG TGAAGTCCAT GCTGAGGAAG CGTTCTTTG
 1551 GGAACCCGTT TGAGCCCCAG GCACGGAGGG AAGAGCGATC CATGTCTGCT
 1601 CCAGGAAACC TACTGGTGA AGAAGGGTT GGTGAAGGGG GCAAGAGCCC
 1651 AGAGCTCCCC GGCCTCCAGG AAGACGAGGC TGATCCTGA GCCCTGCAT
 1701 GCACCCAGGG CCACCCGGCA GCACACTCAT CCCGCGCCTC CAGAGGCCA
 1751 CCCCTCATGC AACAGCCGCC CCCGCAGGCA GGGGGCTGGG GACTGCAGCC
 1801 CCACTCCCGC CCCTCCCCCA TCGTGTGCA TGACCTCCAC GCACCGACGT
 1851 CCAGGGACAG ACTGGAATGT ATGTCATTG GGGTCTTGGG GGCAGGGCTC
 1901 CCACGAGGCC ATCCTCTCT TCTTGGCCCT CCTTGGCTG ACCCATTCTG
 1951 TGGGAAACC GGGTGCCAT GGAGCCTCAG AAATGCCACC CGGCTGGTTG
 2001 GCATGGCCTG GGGCAGGAGG CAGAGGCAGG AGACCAAGAT GGCAGGTGGA
 2051 GGCCAGGCTT ACCACAACCG AAGAGACCTC CCGCTGGGGC CGGGCAGGCC
 2101 TGGCTCAGCT GCCACAGGCA TATGGTGGAG AGGGGGTAC CCTGCCACCC
 2151 TTGGGGTGGT GGCACCAAGAG CTCTTGTCTA TTCAGACGCT (SEQ ID NO:1)

FEATURES:

5' UTR: 1 - 172
 Start Codon: 173
 Stop Codon: 1688
 3' UTR: 1691

FIGURE 1A

Homologous proteins:

Top BLAST Hits

		Score	E
gi 1836161 gb AAB46910.1 (S83194)	Ca2+/calmodulin-dependent pr...	965	0.0
gi 2143629 pir A57156 Ca2+/calmodulin-dependent protein kinase...	959	0.0	
gi 9256525 ref NP_061371.1 calcium calmodulin dependent protei...	946	0.0	
gi 3882295 dbj BAA34507.1 (AB018330)	KIAA0787 protein [Homo sa...	594	e-169
gi 4877951 gb AAD31507.1 AF140507_1 (AF140507)	Ca2+/calmodulin-...	584	e-166
gi 7446417 pir JC5669 Ca2+/calmodulin-dependent protein kinase...	581	e-165	
gi 5729895 ref NP_006540.1 calcium/calmodulin-dependent protei...	577	e-163	
gi 7446362 pir T37317 probable Ca2+/calmodulin-dependent prote...	409	e-113	
gi 7289880 gb AAF45480.1 (AE002612)	CG17698 gene product [Dros...	343	3e-93
gi 3859986 gb AAC72943.1 (AF091074)	unknown [Homo sapiens]	249	7e-65
gi 1711543 sp P50526 SSP1_SCHPO SERINE/THREONINE-PROTEIN KINASE...	231	2e-59	
gi 5053103 gb AAD38851.1 AF156028_1 (AF156028)	calcium/calmodul...	203	4e-51
gi 6320976 ref NP_011055.1 DNA polymerase alpha suppressing pr...	199	7e-50	
gi 6911862 emb CAB72162.1 (AL138649)	serine/threonine-protein ...	193	3e-48
gi 6321259 ref NP_011336.1 Ygl179cp >gi 1170647 sp P43637 KGS9...	188	1e-46	

BLAST to dbEST:

gi|10204347 /dataset=dbest /taxon=96... 555 e-155

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hit:

gi|10204347: Eye (retinoblastoma)

Expression information from PCR-based tissue screening panels:

Human Adult Brain

FIGURE 1B

1 MEGGP AVCCQ DPRAELVERV AAIDVTHLEE ADGGPEPTRN GVDPPPRARA
51 ASVIPG STSR LLPARPSLSA RKLSLQERPA GSYLEAQAGP YATGPASHIS
101 PRAWRRPTIE SHHMAISDAE DCVQLNQYKL QSEIGKGAYG WRLAYNESE
151 DRHYAMKVL S KKKLLKQYGF PRRPPP RGSQ AAQGGPAKQL LPLERVYQEI
201 AILKKLDHV N VKLIEVLDD PAEDNL YLVF DLLRKGPVME VPCDKPFSEE
251 QARLYLRDVI LGLEYLHCQK IVHRDIKPSN LLLGDDGHVK IADFGVSNQF
301 EGNDAAQLSST AGTPARMAPE AISDSGQSFS GKALDWATG VTLYCFVYGV
351 CPFIDDFILA LHRKIKNEPV VFPEEPEISE ELKDLILKML DKNPETRIGV
401 PDIKLHPWVT KNGEEPLPSE EEHCSWEVT EGEVKNSVRL IPSWTTVILV
451 KSMLRKRSFG NPFPQARRE ERSMSAPGNL LVKEGFGE GG KSPELPGVQE
501 DEAS (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDO C00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

147-150 NESE

[2] PDO C00004 PS00004 CAMP_PHOSPHO_SITE
CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

1	71-74	RKLS
2	105-108	RRPT
3	455-458	RKRS

[3] PDO C00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 6

1	58-60	TSR
2	69-71	SAR
3	100-102	SPR
4	160-162	SKK
5	330-332	SGK
6	437-439	SVR

[4] PDO C00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 7

1	26-29	THLE
2	74-77	SLQE
3	82-85	SYLE
4	117-120	SDAE
5	419-422	SEEE
6	425-428	SWE
7	430-433	TEGE

FIGURE 2A

[5] PDOC00008 PS00008 MYRISTYL
N-myristylation site

Number of matches: 2

1	178-183	GSQAAQ
2	326-331	GQSFG

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

485-492 GFGEGGKS

[7] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

134-157 IGKGAYGVRLAYNESEDRHYAMK

[8] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

271-283 IVHRDIKPSNLLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	339	359	0.946	Putative

BLAST Alignment to Top Hit:

>gi|1836161|gb|AAB46910.1| (S83194) Ca2+/calmodulin-dependent protein kinase IV kinase isoform, CaM-kinase alpha [rats, brain, Peptide, 505 aa] [Rattus sp.]
>gi|4512334|dbj|BAA75246.1| (AB023658)
Ca/calmodulin-dependent protein kinase alpha,
CaM-kinase alpha [Rattus norvegicus]
Length = 505

Score = 965 bits (2468), Expect = 0.0

Identities = 472/505 (93%), Positives = 483/505 (95%)

Query: 1 MEGGPAVCCQDPRAELVERVAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
ME PAVCCQDPRAELVERVAI V HLEEA+ GPEP NGVDPPPRARAASVIPGS SR

Sbjct: 1 MERSPAVCCQDPRAELVERVAISVAHLEEAEEGPEPASNGVDPPPRARAASVIPGSASR 60

Query: 61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRRAWRRPTIESHHVAISDAE 120
P RPSLSARK SLQERPAGS LEAQ GPY+TGPASH+SPRAWRRPTIESHHVAISD E

Sbjct: 61 PTPVRPSLSARKFSLQERPAGSCLEAQVGPySTGPASHMSPRAWRRPTIESHHVAISDTE 120

Query: 121 DCVQLNQYKLQSEIGKGAYGWRLAYNESEDRHYSAMKVLSKKLLKQYGFPRRRPPRGSQ 180
DCVQLNQYKLQSEIGKGAYGWRLAYNE EDRHYAMKVLSKKLLKQYGFPRRRPPRGSQ

Sbjct: 121 DCVQLNQYKLQSEIGKGAYGWRLAYNEREDRHYSAMKVLSKKLLKQYGFPRRRPPRGSQ 180

Query: 181 AAQGGPAKQLLPLERVYQEIAILKKLDHNVWKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
A QGGPAKQLLPLERVYQEIAILKKLDHNVWKLIEVLDDPAEDNLYLVFDLLRKGPVME

Sbjct: 181 APQGGPAKQLLPLERVYQEIAILKKLDHNVWKLIEVLDDPAEDNLYLVFDLLRKGPVME 240

FIGURE 2B

Query: 241 VPCDKPFSEEQARLYLRDVLGLEYLHQKIVHRDIKPSNLLLGDGHVKIADFGVSNQF 300
 VPCDKPF EEQARLYLRD+ILGLEYLHQKIVHRDIKPSNLLLGDGHVKIADFGVSNQF
 Sbjct: 241 VPCDKPFPEEQARLYLRDVLGLEYLHQKIVHRDIKPSNLLLGDGHVKIADFGVSNQF 300

 Query: 301 EGNDAAQLSSTAGTPAFMAPEAISDSQSFSGKALDWATGVTLYCFVYGKCPFIIDFILA 360
 EGNDAAQLSSTAGTPAFMAPEAISD+GQSFSGKALDWATGVTLYCFVYGKCPFIID+ILA
 Sbjct: 301 EGNDAAQLSSTAGTPAFMAPEAISDTGQSFSGKALDWATGVTLYCFVYGKCPFIDEYILA 360

 Query: 361 LHRKIKNEPWFPREEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWTKNGEEPLPSE 420
 LHRKIKNE WFPEEPE+SEELKDLILKMLDKNPETRIGV DIKLHPWTK+GEEPLPSE
 Sbjct: 361 LHRKIKNEAWWFPEEPEVSEELKDLILKMLDKNPETRIGVSDIKLHPWTKHGEEPLPSE 420

 Query: 421 EEHCSWEVTEGEVKNSVRLIPSWTTVILVKSMRLKRSGNPFEQARREERSMSAPGNL 480
 EEHCSWEVTE EVKNSV+LIPSWTTVILVKSMRLKRSGNPFEQARREERSMSAPGNL
 Sbjct: 421 EEHCSWEVTEEEVKNSVKLIPSWTTVILVKSMRLKRSGNPFEQARREERSMSAPGNL 480

 Query: 481 LVKEGFEGGKSPELPGVQEDEAAS 505
 L+KEG GEGGKSPELPGVQEDEAAS
 Sbjct: 481 LLKEGCGEKKSPPELPGVQEDEAAS 505 (SEQ ID NO:4)

Hmm search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	275.1	8.8e-79	1
CE00022	CE00022 MAGUK_subfamily_d	45.1	3.2e-13	1
CE00359	E00359 bone_morphogenetic_protein_receptor	26.1	1.1e-06	1
CE00031	CE00031 VEGFR	13.6	0.00033	1
CE00203	CE00203 ERBB_RECECTOR	6.7	0.16	1
CE00334	E00334 urotrophin_receptor	6.6	0.047	1
CE00292	CE00292 PTK_membrane_span	-66.6	4.1e-05	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-81.5	0.0049	1
CE00291	CE00291 PTK_fgf_receptor	-95.1	0.0027	1
CE00286	E00286 PTK_EGF_receptor	-119.5	0.00094	1
CE00290	CE00290 PTK_Trk_family	-132.1	2.8e-06	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-206.4	3.1e-05	1
CE00288	CE00288 PTK_Insulin_receptor	-225.0	0.18	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00031	1/1	243	296	..	1039	1092	..
CE00334	1/1	264	297	..	670	703	..
CE00203	1/1	262	307	..	852	897	..
CE00359	1/1	271	320	..	272	325	..
CE00288	1/1	179	382	..	1	269	..
CE00291	1/1	128	382	..	1	285	..
CE00290	1/1	129	390	..	1	282	..
CE00286	1/1	128	403	..	1	263	..
CE00292	1/1	128	405	..	1	288	..
CE00287	1/1	128	407	..	1	260	..
CE00022	1/1	247	409	..	118	283	..
PF00069	1/1	128	409	..	1	278	..
CE00016	1/1	64	481	..	1	433	..

FIGURE 2C

1 CCGCCCGCGC ATCCATCTGG GCCTCAGCGT GTCCCGAGCA ATCACAAACAG
 51 CAGCCGACA ACAACAACTC ACTTTTACGG CCTCCTTAGT GGCAGGCACT
 101 GTTCTGAGCG CCTTACGGC GTTCCCTCCT CAGCATCTCA CCACGTGCGG
 151 TGAGGTGAGG CCCGCTAGAA CCCCATCTTG CGGGCGAGGA AAACCCAAGG
 201 CACAGAGGCC AAGCCACCTG CTACAGGGCT CCCAGCCAGG AAAGGGTGCA
 251 GCCTGGCTGC CTGGCTTAG AGCCTGGCG CCAAACCGGG TAACAGGGCT
 301 CAGGCTGGAA CAGGAAACCT TCTGCCCCGA CTIGCTGGGT GACCCCGGGC
 351 CCATCCCCAC CGCTGGCC TCCCTCTACC TATCTAAGAA AAGCAGGGAA
 401 AGGTGTTCAA GGGTAAAGGA GGATGGCCTC TTGCTGGAAT GGCAACCTCA
 451 AGGAAAATACG CAAATTATAT GGGCCCGGGC AGCCTGTGGC TTCTGCCTGT
 501 GGCGGCTCG AGTCCCCTAG TCCCTGCCTA GGGCCAAAAAA GCAGGAGCTC
 551 CTGACTCTGG AGTCATTTCT GTTATATGTG CTGGGGCCTG AGGCTTGCTG
 601 GGGTTGCCTC TCTGAGGCTG CTTTCTCATC TGTCTAATGG GGACAGGGCT
 651 GTAACGATCA CTATGGCAAC CACTCATTTA TTCAACAAAT ATTTATCGAG
 701 TTCCTATCAC ATGCCAGGCA CTGATGATCT TTTGGAGACA AGGCAGATGA
 751 GCGTCCTAAT CTATGAAAC TTACATTCCG GAGGGAAAAAA CAAGGCATGC
 801 GGAGGTGAGGG GAAGGGGGCGG AGGGGTGGGC CACCTGCTGG GAGGAGCCTG
 851 GCGGGTCCCTG GAGGGTGTTC CCAGCTTTGG CTTCTCCTT CCTATGCTGT
 901 CTGGTTTCCA AGCTCTCCCC GAAGCTCCAG CCCCACTCAC TGTCCCTCTC
 951 ACCTCCTCCA GGGAGGCCCT CCTATGCCAC AGCCTCTCAC CTCCCTGGG
 1001 GAGGCCTCTT TATGCCACAG CCCCACTCTC TGCTCTCTC CACCTCCTCC
 1051 AGGGAGGCCT CCTCTGTGCCA CAGCCCCACT CCTGTCCCC TCTCACCTCC
 1101 TCCAGGGAGG CCTCTTTGTG CCACAGCCGC ACTCACTGTC TCCTGCCCTC
 1151 TCTTCCAGGG AGGCCTCCCT GATACTCTAG CCTCACTCAG CCTCCTCACC
 1201 TCCTTCACCT CCTCCAGGGA GGCCCTCTTG ATGTTCCAGC CTCATTAAC
 1251 CCCTCTCACT CCTCTGGTC CAGCTTCCAT GACTTTCTC GTTCTAGTG
 1301 TGGAGCCTCC TCTCTTCTT TCTCCATGTC AGCACCAGCC CCACCGCCTC
 1351 CAGGCTTCTA CTCAATTCAAC ACACTGCGTA CGGGGCACAG GGGGTCTGGA
 1401 CCTCACCTT ACCCTCAGTC TACCTCCAAA CCCTGCTGTG AGCCTGGAAA
 1451 ATATGGGAAG GCAGGGAAATC CACAGGACAA GTGGGGAGAC TGGGGCTCAG
 1501 AGTCGGGAAG GAGCTGGTCT AGGGCCCTG GTGGGTCAAGC AGGCAGGACT
 1551 GGAACCCAGT CCTGGCTCT CAGTGGCCGG TGGACTCCAG CCAGCCCTGC
 1601 CTCGCTGACA TCTGTCAAAG CAAGGGGATG GGGAACGAGC GGTAGAGCAG
 1651 GCGCTTCACC ATGCGTACTC TGGGTCTCCC TGAGACCCAT GTTCTCAGTT
 1701 GCTGTGTGGG TTCGGAGGAA GTTACACAGCA GACAGGAAGG ATGGAGGGTC
 1751 AGGAGTTCAC TCACTTCTT CTCCGTAGAA CATGCAGAGT CCAGCGCAAG
 1801 CAGGGGAAG GGCATCAGGT TGGGCATGGC CAGCGCTCTA CAAGCCTGGG
 1851 ACAGAGATGG GGGTCTCAGG CTGAGTGTCA GGGTTCACTC CGGGGTCAAG
 1901 ATGTAGCCCA GGGTCATGGC TGAAGGTGAG GGCTGGGGGT CACCTCCCTG
 1951 ATGTTTCAGC CGCCACACAG TGAGTTGAG AACATGAGTC TCAGGGGATG
 2001 TCATGCCCTT GTTTCACCCC TCATCCCCCT CATTCCCATC CCCTTGCTTT
 2051 TTTTGAAAC CGAGCTTTCG TCCATCACCC AGGCTGGAGT GTAGTGGCGT
 2101 GATCTTGGCT CACTGCAACC TCCACCTCCC AAGTTCACAC GATTCTCCTG
 2151 CCTCAGCCCTC CCGAGTAGAT GGGATTTCAG GTGCACGCCA CCATGCCCTGG
 2201 CTAATTTCAG TATTTTTAAT AGAGACAGAG TTTTGCATG TTAGCCAGGC
 2251 TAGTCTCGAA CTTCTGACCT CAGGTGATCC ACCTGCCTCG GCCTCCAAA
 2301 GTGCTGGAT TACAAGTGTG AGCCACCATG TGGGGCCCAT CCCCTTGTT
 2351 TGACAGACGT CAATGAGGCA GGGCTGGCTG GAGTCGGGAG CCCCAGGGAA
 2401 GTCTTCTGGG AAGCAGTGTGAG AGGGATGGGG GTAGGAGGCT GAAACATCAA
 2451 GGAGGGCTCC CTGGAGGAGG CGGGTGGTC TGAAGCATCA GCAAGGCTTC
 2501 TGAGTTACTA GTGTCTAGCT CAGCTTCCAG GAGGCAGTGT CGGAGTGCTC
 2551 TGCTGTCAAG GGTGGGACT CATGACTCAC AGGGCTGCAT GCTGTGCTGG
 2601 GGCTGAGCTG ACCCTGGCT CTGCCCCCTC CAGTGCTGCT GGGCCTCCAG
 2651 GCTTCTGCCCT TGTCTGTCT GATTCCAGAA TATCAGATTG TCTCTGCTTC
 2701 CCTGTGAAGC CAGCAGGCCAG AAGTGAATGC CTCTGTTAAC GGCAGGGATA
 2751 CTGAGGCCAA GAGGGCTGGC ATGGGGCAGA ACCGATGTGA ATTCAATTGAG
 2801 GTCATAGGAA CAGACTTGAG TTTGGGTGTT GGCAATCCCG GTAGAGGGAA
 2851 CAGCCAGGGC AAAGGCATGG AGGTGGGACCC CACAGCGCTG TGGCTACCTT
 2901 ACCTGGTAGC CAGCCTGACA CCCAGGAGTG AAGCCTTCTC TGCCCTCTT

FIGURE 3A

2951 TCTCAGGTT CCAACAAGGC TACGGCAGAAG AACCCCCCTTG ACTGAAGCAA
 3001 TGGAGGGGGG TCCAGCTGTC TGCTGCCAGG ATCCTCGGGC AGAGCTGGTA
 3051 GAACGGGTGG CAGCCATCGA TGTGACTCAC TTGGAGGAGG CAGATGGTGG
 3101 CCCAGAGCCT ACTAGAAACG GTGTGGACCC CCCACCACGG GCCAGAGCTG
 3151 CCTCTGTGAT CCCTGGCAGT ACTTCAAGAC TGCTCCCAGC CCGGCCTAGC
 3201 CTCTCAGCCA GGAAGCTTTT CCTACAGGGAG CGGCCAGCAG GAAGCTATCT
 3251 GGAGGCGCAG GCTGGGCCCT ATGCCACGGG GCCTGCCAGC CACATCTCCC
 3301 CCCGGGCTG GCGGAGGGCC ACCATCGAGT CCCACCACGT GGCCATCTCA
 3351 GATGCAGAGG TTGGTGGGGC AGAACGAGGG GTTGTTCATG AGCCCCCTCAG
 3401 TAGTCTGCAA TGAAGACTCT TTCCTGCCCT TGCTGTGCC ACACGGCTAT
 3451 CTAGCTTTGG TTTGCATACC CTCAGAGCTG GGGAGATCAC TACCTAACAA
 3501 TATAGCTTCT TCCCAACCAG GGGAGCTCCA GCTGAGCCAA AGGCTGCCCT
 3551 CCCTAAGTCC TGCTATTCCC ACTCCCAGCC CAGGCCCTAGG AAATAGGTCT
 3601 CTCCCTGGTC CCCTATGTAG TCTTCTTAGA GATGTGAAGA TAGATGCTAT
 3651 GTCCCCCTTC CCCCCTAACT CTTCTCCAGC TTGCACCCCT CGCCTCTAAT
 3701 TCTGCCCTT AGAGTCTGCT GTGACTCAGA AGCGGGCCGGC CTGCCTCCAG
 3751 CCTCTGGGCT TCTGCTGGAG TTCTTGCCAT TTAGGTCTGA AAGTGAACTC
 3801 AGGTCCAAG CAGTCTACAG ATGTCAGGGG CTGAGCTTTC TGTCCTGAA
 3851 CCCAGGCTCT CAGCCTCTGT GCCCAGGGCT CCTCATCTTG TCCTTGGAGT
 3901 CTAGACCTTC TCATTCAGCT GCTTCTGGAA ATAGTTGCTC ATGGGTTTCT
 3951 CATGGATTAG GGTCCTCCAG ACTCCAGAAT CCAGACAGGA ATTAGCGTTT
 4001 TCCCCTCACC ACTGCTTCTG GGGAAACAAGG CACAGCCATG GCGTCACCAT
 4051 CCATGTTTTC AAACATGAGC CACGCTTCT CGTCACATAC GGGGGCGATG
 4101 GCACCACAA CTTCCCCATC CAAACTCAAA AGCTTGGTGA GACCTGGGGG
 4151 TCGGGGAATG AGGAGCTTAT GGCCAGAATT GGACCCCTGAA CGGGCTCTGA
 4201 GGTAGGAGCA GTGCTGCCCT CGGACCCAGC TCCACCTGGT GCTCGCTCTT
 4251 CCCCCACAGG ACTGCGTCA GCTGAACCAG TACAAGCTGC AGAGTGAGAT
 4301 TGGCAAGGTA GGAGTGGCA GGCGCAGAGC AGTGGGGGCT TCGGGATTCT
 4351 CTGTTGGCG CTGCTCTTC TCTCGTGTGG GAGGGAAACGG GAGGCAGAGC
 4401 CAGGCAAGTC CTAGCCTGGA GGTGAGGACA GTTTCGTGCC CTGTCGGAG
 4451 TACCCAGGTA CCCAGGGGGA GGGTGGAAAGA TGGCTCTGA TTCCCGACTC
 4501 TCTGAGTTCT TGACAGTGG CAAGGAGGGG CTGAGGGAGG CATGGAGCCA
 4551 TGTGGAGCCA AGCAGGGGCA GTTACCCAGGG CGCAGGAGTC CCCTCCCCAT
 4601 CTGCTACAAT ATTTGCCCGT GAGCCAGCTG GTGGTGGGTA GTGCAGATGG
 4651 GGTGCAGGAG AGACCAGAGC TGCTCGGCTC CCCACCTCCT GAGCTGGTCC
 4701 TGGGAGGGGT TGCCCTGTCC AGGTGGGGCT GACTGATGCC TATCTGCAGG
 4751 GTGCCTACGG TGTGGTGAGG CTGGCCTACA ACAGAAAGTGA AGACAGACAC
 4801 TATGTGAGTC TGGGGATACT AGGGAGGTGT TGCCCAAGCC AGGCCCTGGA
 4851 AGCCTGAGGG GTGGGGCAGG AGTTGTGCTT AGGAGATAGA GGACAGGGCT
 4901 GCCTGAGGT GAGCTCCCTG TCCCTAGGGG TATGCAAAGG AATGAGCTTC
 4951 CTAACCCCTGG GGATATGCAA GCAGAGACTG GATTCCTCTG AGGGAAAGC
 5001 TCCAGAAAGG CTTGCTGGGG GAATAAGGGG AAGGGCTAGG CTCAGATATG
 5051 GCCACCCCCA ACCCCGCTTA ACACCTACCT GGGCCACACC CTCAGGGCCA
 5101 GTAGCAGATG TCCAGTGTGC CTCTCCGGAC CTCACTCCAC ATGTACCAAGC
 5151 CTGTTCTAGC CCCTGGTGGC TGACAGTAG TGACATTCT GTCCCTCCTT
 5201 CCTTACGCAA TGAAAGTCTT TTCCAAAAAG AAGTTACTGA AGCAGTATGG
 5251 CTTTCCACGT ATGTATCTTC TGATCCTGTG CCTGGGAGCT CCTAGCCTGG
 5301 AGGAGAGGA GGAGACCTCG ATCCTGAGCT AGTTTGGCT AGGAATGGGG
 5351 TAGAGAGGGA GACAGCGTGA GCAGAGGCCT GGGGACAGAA TGTGCCCTGT
 5401 GGGTTGGGAC AAGACCACGG GCATGCAAGA CTCTTGCTTG AGACTGGTTT
 5451 GGGGGCCACG GTGAGGCCA GCCACCTGGA ACAGGTGTTT GAGTTCTTT
 5501 CCTGGTCACA GGTGCCCCCTC CCCCCAGAGGG GTCCCAAGGCT GCCCAGGGAG
 5551 GACCAGCCAA GCAGCTGCTG CCCCTGGAGC GGGTGTACCA GGAGATTGCC
 5601 ATCCTGAAGA AGCTGGACCA CGTGAATGTG GTCAAACCTGA TCGAGGTAGG
 5651 GGGTGGTGGT GAGCAGGTGG GAACCAGCAC CTGAGTCTCA TGGGAGCCGC
 5701 TTCTGGTGCT GGGGAGCCCC TAGCACAGAC CCAGGGATCT TGCCCAGGTG
 5751 GCAGATGTGG CTGAGGCCCT TGAGGACAGG GCCAGACTTG GGGTGGGGCT
 5801 GCAGGAAGGC TTGGGGGCC CAGCCTGGTC AGGGATGTTC CCAAGTTCCC
 5851 ATGGAGGGTG AGGGGCTGCC CCAGAGGCAA GAAGTGAGCC CCTCATTGCA

FIGURE 3B

5901 GCTGGAGGGG AGGAAGGCTG GATGTCGTGT GGCGGGCCAG GTTGGGGTC
 5951 GGTGACTTCT GAGGCCCAT CAGTCTGGCA CCACCTGTAC ACTTCCTGCT
 6001 TCCTTGTCTG GGGTGGTTGC ATGCATACTA AGGGTTCTGG GGCTGGCAAG
 6051 GACCAGGAGG CCTGGGACCT CCAACCCCAC GCCTCCTCAA GCCCACCCCC
 6101 CATGCTGCT CCCTCTGACC AGGTCCTGGA TGACCCAGCT GAGGACAACC
 6151 TCTATTGGG TGAGTGACCT GGCTCATTCC CACAGCAGCT CACTCAGGGC
 6201 TGGCCAAGG GCTCCCTTGG GACATGTATG ACCTTCAGGT GGGCGGTGTA
 6251 AATGCACTGA CCTCCTGGG ACAGAAGAAA AACACACGTT CTGAAGCCCT
 6301 GGATTCCCTT GCCCAGCCCT GCAGAACCCAG GCCCAGAATA TCCAGTTAGA
 6351 TTCAACAAAT ATGCCAAGC CCCACTCCCT GCTTCCCTCT GAGCAGCAAG
 6401 ACAGTGGATC CAGTGGCT GCGCGCTAG GTAGATGCAG GAAGCAGGCT
 6451 GCATGGGTTC CCAGACACTG TAGCTCTGTG CCTCAGTTT CCCACCTATA
 6501 AAACAGGGAT ACTAGTGGTG TCTACCTCAT AGGGTTCCCTG TGAAGAGTAA
 6551 ATGAGTAATT ATATGTAAG CACATTGTT ATTATCCTTG TTAATAGTAA
 6601 TGTTATTATT TTAGTTCCTT GTGTCGGTT CAGGGCTGGG CTTAGAGGAG
 6651 GCCTCAGAAA ATGGGGCAGA AGAAGAACTG GCTTAGGAAT TAGAGGCTGA
 6701 GGCTTCTGTC TCCACTCCCT ACCCTACCTG CCTGTCGTCT ATGACCTTTA
 6751 GGAAAATTC TGCCCTTCT CTGTCCTCA GTTTCCCTCT CTGAAAAGG
 6801 GCCCCATGCT GATGCTGATG GTTCTCACCT GGCACCTGAG GATCAGATGA
 6851 GACAGGTCCA TAGCAGACCC CACTCTCATG CATTATTITG CTCTCATATC
 6901 CCAGGGTCCC CTGTCCTGTC CCTGCCTCGA GTATGCCTGC ATGCCTGCC
 6951 CCTCTCCTAC CCTCCAGAAC AGGGAGGGAC CTTGGCATCG GCTGTTTGC
 7001 CAGCCAGCTA CACCTTACCT TCTTGTCTT TCTTTCAGTG TTTGACCTCC
 7051 TGAGAAAGGG GTGAGTTCCC CGTCCGTGATC AGGCAGGTCA ATTCTCATCC
 7101 AGGCCTTCCT TCCCTTCCCT CCCTGTGTCC CCAGCCCAAGG GTCAGCTAC
 7151 TCTAGGAGAA GTCAGAGACG GAGGCCCTGC CTTAGGGGT AAATAAGAGA
 7201 CCAAGAGGAC CATTCTTGA AGGCTGATGG GGGTCAGTGA GGCTGAAATA
 7251 GTCAGGGAGA CCTCTGGAAA AGGGGACCGGA TTTTGACCCA GGCCTGAAG
 7301 AACTAGGAAG ATAGGGATGG AGGAGAGGGG GAAGAAAGGA GTGTTTTTA
 7351 GGTAAGAGTA TATAGAGGTG GGACTCAACT CTTACCGGTAA TTCAAATCAC
 7401 AAAGGGTTT TCAGCTTCC AACAAGTCTG TGAATGGAGT GGGTGGGATT
 7451 CCAGTTGTC CCAATTGTGA GAGGGAAAGC TAAGGACCAAG AGAAGGTACG
 7501 TGGCTTGCTC AAGGTACAC AGCAAGTCAC TGATGGAGCC CAGGTTCCA
 7551 CATGCTGCCC CTATGCCGT TTTCAGGGTA TTTACAGAGC AGATGACATG
 7601 GAGTAATGAG CACGGGGCTG GGTGGTCCCG GACCCTCACT GCCAAGGCTT
 7651 GAATGCAGCC TGCGGCTTGT CCCTTGCCT GGGCGGCTCC CTACAGACCA
 7701 ATCTGGGAG AGGGCAGGG AGTGGTGTCC CTTTAAGACT TGGAGGCTTT
 7751 CAAATTTT GACCTCTATC CAAAACAAGA AATATATATT TCTATTGCTA
 7801 TCCATATCTG TAACTGAAAC CAAATTGTTA CAAAGCAGCA TATATCTTTA
 7851 CTACATGAA TATATTCTGA TATATTCTAC TTATTTAGGA AAAAAAAA
 7901 AAAGCAGTTG CCACCCACTA AATTGATTTA ATGATCCTCT CTTGGGTCTG
 7951 GATCCACGGT TTGAAACAGT GCTCTAAATG GCATCTTGC AATTGATTAT
 8001 GGACAATTAA GTACTTAGAA GAAGGAATAT CAAGCCAATC AGAAATTAAG
 8051 AGAAAGCTGA TTGAAATTAA TGATTGAAAT GGGATATGTA TGAGTATGTG
 8101 TGCTTTAAGT TTTTATTAT GTAGCAGAAA AAGCTAATAT CTTGAGTTGT
 8151 AGGGACTCAT GTGGGCACAG GTTTCGGGG ACCTCCCGAC CACCTGAATG
 8201 GCGGGGTGCC CTGATTTCACT CTGAATGCC CTCCTCGCAT CTTCTCCAT
 8251 AGGCCGTCA TGGAAAGTGCCT CGTGACAAG CCCTTCTCGG AGGAGCAAGC
 8301 TCGCCTCTAC CTGGGGACG TCATCCTGGG CCTCGAGTAC TGTGAGTGC
 8351 GGGCAGCTTG CCCACTGGGG CTGGGGCTAG GGGATCTGGC AGGCGGCAGA
 8401 GCCCAGGCTG AGCAGACTCT GAGCAGCTCC CGTCAGTCAG AGCTGACCTG
 8451 CCAATCAGCT TCAGTGGAG TGGGGCATGC ACCTGTTGGCG GGGCAAAGG
 8501 CCTTTTGTG GGGTGGGGCG GGCAGGTGGAC TCCACTGGGC ATGTGCCAGA
 8551 TCCTTCGTG TGTCGGTCC TGTGGGTCTG AGTCCTGGCT GTTCTGTATC
 8601 TTTCTCTGC TGAGTTCTTA GCCTAGCTTA GCGTTGCCAC GGGGCTCAA
 8651 GAGATGTGGG AAGGAAGGGA TTATGTCCA GCTGCTGGGG AGAGTCTGTC
 8701 CTGGCATGGG GCCGGGGCAT GGTGGCAGGG TGGATTTACC TGTGAGGGGC
 8751 CCTAGTCTGA TAAGAGCTCA GGAGGGTGAT GTGAGCTTGG CCTCTGTCTC
 8801 ATTCATTCA TTAGCTACAT TCACTTGCCT GGGGGCATAG GGGTGAAAGA

FIGURE 3C

8851 CCCAGACCGG AGTTCACGGC CTAGTGGGAG GGACAGGAAT CTAGGCAGGC
 8901 AGATAATACA CGCTGGTGCC TGCCAAGGCT GGGGAGCCTA GAGGTGTTAG
 8951 GAGTGCCGGG GGGCTGGGGA AGTCTCCCTG AAGAGGCTAC TTATGATTCTG
 9001 GGTCTTGAGG GATGAGTAGA CTTCCCTGCT CAGGTTTGA GGGATGGCG
 9051 TGGAAAGACGA TGTGCCCTGGC ATAGGCCTGT ACTCTGAGTC TGGGGAGAAG
 9101 TGGAGTCTGG CTGAAGCCTC CAGTGGCAG AGGAGGGCCG TGGTTAGTGA
 9151 AAGATGATGC TGGAAACACT GTCCGGGCCA CAGCATGAGG GCTGGAATC
 9201 CCTCCCCCTGA GGTCTTTGCT GACTGCATCC TGCCAGCTCT GTGAGGCCCT
 9251 GAGAGTTTA AGCATGGGA GGGGGCTGAT GGGATTGTG CCTGAGAAAG
 9301 CTCTGTCTGG CAGCTGTG TGGGCTGGAT TGGAGTGTGT CATCGGAGGG
 9351 TGAGAGGCAG CCAGCTGCC AGGGAGGAGG CTGTTTCTGC AGCCCAAGTG
 9401 ACAGATGGTG AGGCCTGGAT TAAGGCAGTG GCAGCAGGAT GGGGATAGGA
 9451 AGGAGGTGGG GTGGTCAGCA TGGAGTGAAT TGCCGGTCTG GGGAGGAGGAG
 9501 AGCCCCTAGA CACCTAGGGT CCTGGCGTGG GTTGGGGACC AGGGGAGATG
 9551 CCCATCTCTA AAATCTTAGC TTGGGCCAGG CGCAGGGGCT CATGCTGTA
 9601 ATCCCAGCAC TTTGGGAGGC CGAGGTGGGT AGATCACCTG AGGTGAGGGG
 9651 TTTGAGACCA GCCTGGCCAA CGTGGCAAAA GCCTGTCTCT ACTACAAATA
 9701 CAAAAAATTAG CCTTGTGTGG TGGTGGCAC CTGTAATCCC AGCTACTCGG
 9751 GAGGCTGAGG CAGGAGAAC TCTTGAACCT GGGAGGTGGA GGTTGCAGTG
 9801 AGCCGAGATC ACGCCATTGC ACTCCAGCT GGGTGACAAG AGTGAACACTC
 9851 CATCTAAAAA TAAATAATAA AATAATGCA TACATACATA TATACATACA
 9901 TACATAAAAAA TAAAAAATAA AATCTTAGCT TGTTTCTTG GGAGCATATT
 9951 CTTTCCCTGG GGGAACAGGG TGGGGATCTG GCTGAGGTTT GACCTGCAGT
 10001 GACAGAAACA GGACTGTCTT TATCCTGCTC GAGCCTCTCC TTTGCCTTCA
 10051 GATTAAGACT CTCTTGAC ATATGGGAA ACTGAGGCAC ACAGAGGGGA
 10101 GGGCTTTGCA GAAAATCCCT ACCAAGGGCC TAGAGGCATG GGATGGGAAG
 10151 GGGACATTTT ACCCCGGTAC GTCACTGGC AGGCACAGTC CTGTACCGC
 10201 TTGGCTCCAC CTCTTTCTG TTGTAGTCCC TTCTTTCCCC TGAAGTCCTG
 10251 TTGTCAGCTA TCCCCTAGCC TCCACAAAGA AACGAGTTA TCTTACCTGG
 10301 TTCTGGGTA AAGCCTCATC AGGACCCAGC TAATCACAGT GAAGGGCTTC
 10351 CCTGGGGCAG AACGGTTAGC GCCAGGGCT GGACAGGTGG ATGAACAGAG
 10401 GCACGAGGGC GCTGAAGACC TGCCCTGTGA TTCTGGCCCC AAGAAGAGAG
 10451 AGTTGAGGCT GCCATGAGAG GGCTCGGTGG TCAGGGCGC CCAGGCCTGG
 10501 TTCTCAGTTG ATGGGGGAG GTGCAACGAT GCAGATGATG AGAACAGTT
 10551 GGATCTGGAA TAGATGTGAG AAGCTGAGCT CACAGACCTT GCTGATGAGC
 10601 AGGATGTGGG GTCTCAGAGG AGGAATTGAG GATGATCCTG AAGTTTTGG
 10651 CCTTTCACAG AATGGAAAAG AATGGGGAGC AGCAGGGGCG TTTTGTGTTG
 10701 CTTTGTGTTG ATTTTGTGG TGTTAGGCAT TGCAAGGAGA GAAATCAAGT
 10751 TCTGAATTAG ACATGTATT GCACTGTGTT CAGATATACA GAGACATATA
 10801 TCGATGCCA GCTGCCTAGT TATCTACAA GATGTCATT GGAAATCTAT
 10851 GTGGGTAAAG AGCTGGAGTT CAAGGGAGAG GCTAGGGTTT GAGATAAGAA
 10901 CATGAGACCA CTTTCCATGG TCAAATGTCC ACCCCCCCTGA GCTTCTGTGC
 10951 CCTGAAGGGT GTGTCAGATT CCTTGTGTGT GCCTGGCACA TAGTAGGCAA
 11001 TCAAGAAAGT GCCACTGGTT TTATGGTTAT TGTTATACGG CACCCGCCCT
 11051 CTCTGCCCGC AGCCTCCCTC TCCTCTTCTC CCTTCTCTT TCTTCTCTCG
 11101 CCTTCTCTCC TCCCTCCCTC CCAGCATCCT GGGGTCCGTT GGTCCAGATG
 11151 AAGGTACTTG CCAAGGAGGG AGCCACAGG TCGATGGTCG CGGGATGGGG
 11201 TCAGTGGGGT CATTGTCTCT CTTGGCTGGG ACCTTACCAAG TCATGTCAGC
 11251 TTGAGGCCACC TGTCACTTCG TGTTGGTGCT GGGCCCAGAA AGCAGGGCAG
 11301 ACCTCCAGCC TATTAGGTCA TTTCTGATTT GGGATTCGTC CTACTATATG
 11351 TGGCTGACCT TACACCCAG CTGTCATC TGCTTGTCC CAAGGCCCTGG
 11401 GGTGCCATCC ATCTCTCTGA AACCCCCATCA GCCCAGATCC CGAGGGCTGA
 11451 GATGGTACCT CTGAGGATA GCAGAGTCCC TACAATCTTA CTCTCAGTCC
 11501 CAGCAGCAGG GACATCTTTG CCTAGCCTGG GTGGGGGATG GAACTGGAGA
 11551 AAGGTTTGA TTGGCTTTGG GCCTGCAGAC GGCACTCACA GGGAAAGGGGC
 11601 AGAGCTAGCC TAGGAAGAAC TCTGCTCCA GCTGGGGGGCG GTGGCTCACG
 11651 CCTGTAATCC CAGCACTTTG GGAGGCCAG GTGGGTGGAT CACCTGAGGT
 11701 CAGGAGTTCA AGACCAGCCT GACCAACATG GCGAAACCT GTCTCTACTA
 11751 AAAATACAAA AAGTAGCCGG CGCTGGTGGC AGACACCTGT AATCCAACT

FIGURE 3D

11801 ACTCGGGAGG CTGAGGCAGG AGAACATCTTT GAACCTGGGA GGTGGAGGCT
 11851 GCAGTGGGCC GAGATCACGC CATTGCACTC CAGCCTGGGG GACAGAGTGA
 11901 GACTCTGTCT CAAAAAAA AAAAAAAAC CAAAAAAA AACAGCAACA
 11951 ACTCTCCCTGC CCTAGTTCC TCTGACCTCC CCACTCAGCA GCAGATCCCT
 12001 TGTTTGTAT GGAGAGGGTG CTGGACTTGG AGTCAAAGA CTCCTAAGAT
 12051 TCCAGTCCTG GCTCTGCTGC TCACAGCCTG GGCTCAGTGT CTGCACCTGC
 12101 GTGGAGCAGA TGGCCCTGAC GTCCCTCTCC CAGGTCGTCA CCAGACGAAA
 12151 GTGTGCATGG GCTGGGATGT CCCGGCCGGC GTCCCTGGCT GTGCAAGGAC
 12201 GGGTGTGGGG TCCCTGGCCAG CGGTGCCAG GCCAGCGCTC AGCTCAAGCT
 12251 CCCCTTCTCT GCAGTGCAGT GCCAGAAGAT CGTCCACAGG GACATCAAGC
 12301 CATCCAACCT GCTCCTGGGG GATGATGGGC ACGTGAAGAT CGCCGACTTT
 12351 GCGTCAGCA ACCAGTTGA GGGGAACGAC GCTCAGCTGT CCAGCACGGC
 12401 GGGAAACCCC CAATTCACTGG CCCCCGAGGC CATTTCCTGAT TCCGGCCAGA
 12451 GCTTCAGTGG GAAGGTGACT CGCAGGCCCT GGGCCAGGCT GGGGTTCAAG
 12501 TGGGGGGCGT AATAGCTTGC CGCAGTGGCC CAGTTTCTAA CCTGAGGGTG
 12551 CCAGGGTCTT TGTGTCTAG GAGTGCACATA TTTGCCTCTT CCTGGGAGCC
 12601 TGACAAACTC CACAACCTTG GCCTCTCCT GTTTCCAGC AAAGTGGTCC
 12651 CAAATCTCCC TTGAGATAT TTACTGTTGG TTGCTCTGTG CTGGGTTCTG
 12701 GACCGGACTG TGGAAAGAGGC AGAAACAAAG AGAACCCCTGT TTCTGCCCT
 12751 CTGGATGGTT TCGGGGGAAAG TTGGGGGTCC CCGCAGATCT TGGGACATGG
 12801 CAGGATTTGA ACTGGCCCTT GAAGAATGGG GAGGATCTGA GCAGGACCTG
 12851 GAGCCTAGAG AATAAACCG AGAACAGAAAG GGCTCAGGGT GGGGGGCAGA
 12901 GGGTATAAAG GGCCTGGAAG TTTGGGCTTT CTCTTAAGTG ACAGGAGCGT
 12951 AGGAAAGTT GTCTGAACAA GAGGTTACAC GGTCTGGCGC AGTTCCCTGG
 13001 GCACATGGCT GTTTCACCTA TGGAGTGCCA GCCACCCCCAC TGCCAGGGAG
 13051 GCTGTGGGTG AGAGGCATTG GGACACGTGT GAGTATCCAG GAAAGAGGTC
 13101 AGGAGGCCGG GCACAGTGGC TCATGCCCTG AATCCCAGTG CTTTGGGAGG
 13151 CCAAGGTGGA TCTCTTAAGG CTAGGAATTG GAGATGAGCC TGGGCAACAT
 13201 AGCAAGACCC CATTTCCTACA AAAAAAAA TAAAAACATT AGACAGGTGT
 13251 GGTAGTGCAC ACCTGTAGTC CCAGCTACTT GGGAGGCCGA GGTGGGAGGA
 13301 TCGCTTGAGT CCAGGAGTTG GGGGCTGTAG TGAGCTGTG TGTTGTCTAG
 13351 CCTGAGTGAC TGAGCGACAC CTTGCTCGA AGAAAGAAAG AAAGACGTTG
 13401 GGGATGTTGA TAAAGATTIT TTGAAATGTT TTATTTGAT ATAATTCTAA
 13451 ATTTACAGAA AAGTTGGAAG AATAGTACAA AGAAATCCCC TATATCTTTT
 13501 TACCCAGATT CACCAATTAT TGACATTITG TCCCACCTGGC TTTTCATCA
 13551 TCTTTCTTTT TTTTGAGCC GGAGTCTCGC TCCGTGCGCC CAGGCTGGAG
 13601 TGCACTGGCG CGATCTCAGC TCACTGCAAG CTCCACCTCC TGGGTTACG
 13651 CCATTCTCCT GCCTCAACCT CCCGAGTAGC TGGGACTACA GGCGCCCCACC
 13701 ACCACGCCCG GCTAATTITTT TGTATTITTT AGTAGAGACG GGGTTTCACC
 13751 GTGTTAGCCA GGATGGTCTG GATCTCCTGA CCTCGTGATC CGCCCCCTC
 13801 GGCCTCCAA AGTGTGGGA TTACAGGTGT GAGCCACAC GCCCAGCCAG
 13851 AAATTATCA TTGATAAGAC TTATATATCG GTCAAGCATG GTGGCTCATG
 13901 CCTGTAATTG CAGCCCTTTG GGAGGCAAG GTAGGTGGAT CACCTGAGGT
 13951 CAGGAGTTT GAGACAGCCT GGCAACGTG GTGAAACCCC GTCTCTACTA
 14001 AAAAATACAA AAATTAGCCG GGATGGTGG CGGGCACCTG TAATTCCAGC
 14051 TACTTGGGAG GCGGAGGCCAG GTGGATCACC TGAGGTCAAG AGTTTGGAGAC
 14101 CAGCCTGGCC AACGTGGTGA AACCCCGTCT CTACTAAAAA ATACAAAAAT
 14151 TAGCCGGCA TGGTGGCAGG CACCTGTAAT TCCAGCTACT TGGGAGGCTG
 14201 AGGCAGAAGA ATCGTTCGAA CCCAGGAGGC AGAGGTTGCA GTGAGCTAAG
 14251 ATCGTGCTAT TGCACTCTAG CCTGGGCGAC AGAGTGAGAC TCTGTCTGAA
 14301 AAAAAAAAGA CATACTATAAT CCACAGACCT TATTTAAATG TTATCAGTTG
 14351 TCCTGATACT GTACTTCATA ACTTCTCTT TTTCTGGTCC CGGAATCCAA
 14401 TCGAGGACCA CTTGCTGAT TCACCTCTT GTCTGTGGTA TCCTTTCATC
 14451 TGGAAAGAGGG CCTTGGCTG CCGGTGTCTT TCCTGATCTT GACATTTGG
 14501 AAGACAACCA GCCTGTTATT TTGAGAATG TTGTCAGTTT GCATTGTCT
 14551 GGTGTTCCCT GGTTGGGATT CAGATGATGC ATCTGGGCA GGAATATGTA
 14601 GTAGAGATC GAGAATCACT CATATAAGCG AGAAAGTGG A TACAGAAGA
 14651 GGTGGCGTTC CGGAGCAGAA GGTAGAGAGA GCACACGCTG GAGTCCAGGG
 14701 CGCGGGGAGG CCCAGGGGTG TTTGGGAGCC CAGAGGAGTT GTTGCAGTGG

FIGURE 3E

14751 CGGTGGATGA GGGCGTGAGA GGACAGGGCC TCTGTGTGGG CAGGGGCTGT
 14801 TTGCAATATC AGGAAGAAGG TGGATTATGA GGAGAAAGGG A TGACTCCTTG
 14851 AAGCCCGAGC TGGTTTAGTGC AGCAGAACGTT CCATATATAC CATCATTCCCT
 14901 GGGGTGCGTC TGTGGCACCG GAGCGGCCCG TGTGACCCCTC TGGATGAAGG
 14951 AGGTTTGTA CCTGTTGAGT TGGAAACGTA CCTGGTTAGA GTCTTCCC
 15001 AGGAAACCCA GAACCCCTGG AGGGTGGAGG CCTTGTTCTG GCCGCCCTG
 15051 TGTCCCTCAGC ACTCAGCACG GGGCCCAGCA TCAGGCAAGT ACCGCGGAGT
 15101 GTTTGTGAG TGAGTACATG ACAGAGGAAA GAGGTTCCCT GCAGGCCTCT
 15151 CCTGAGCCCC GCTGGAGCTG GGTGGGCAGA GGTGGCTGTG CCTGTTGGGG
 15201 ACTGATGTGA GCATGTTCT TTCCAGGCCT TGGATGTATG GGCCACTGGC
 15251 GTCACGTTGT ACTGCTTGT CTATGGGAAG GTGAGTGCCTA GGGATGCCAG
 15301 CAGAGCTGGG GCGGGTCCAG TGAGGGGGC ACAGGGCGACG GATGCAGGCT
 15351 CTTCTTTTT GTCTTAAGT GGCTTTGAA AGAGCCCACC TGGCTCAGAG
 15401 AAGGCTGAGA GAGAAGAGGC TTTTCTATC TTTCTCTGGT CCCCTGCCGA
 15451 GCGATTCTCG CGAAGGAGTC GCAGGACAGC AGACACCTAA GGGGAGGTGC
 15501 CGACGATGGT GTGCCACCG CCCCAGCCAG AGTGTCCCC GTCCCTCTGT
 15551 CCCTGACGC CATTCACTTA TTGAGCCATG TGTTCACTCC CTTGCTCATT
 15601 TATTGACAA ATTGTCCTTC ACCCCTACCC TGGCTGAGGC TGGACCCCTGG
 15651 GGACACCCAA CGCTGACGT ACGGGGAGG ATTTCAAGTGA ACATGTTCCC
 15701 TCTGGTGACC ACACAAAGGG GCAGGGGGGA ATTTCAAGTGA ACATGTTCCC
 15751 AAGCCCCAGG CCCTGGAGT GGAGGCCTGG CCACAGGTGG CGGTAATGGT
 15801 GGTGGGTGCA CCCAGCTGG CCTGGCTGG CCGCGGGTGG CAGTAACGGC
 15851 GGTGGATGCA CCCAGCTCA TTGTTCCCTC AGCAACTCAT TCATTCAGTC
 15901 AACATTTGT GAACATTTAC AGTGTGAGTT GAGGTCTTC TCATGTAATG
 15951 GGAGCCCAGA CCTGCCCT ACCCCTGCC CCACCAAGGG AGGGGGTTG
 16001 ATCCCCTGGC ACAGGTGGAG GCCCTGGACC CACATCCTT GTCTGCCTCT
 16051 CCACCCCACA GTGCCCTTC ATCGACGATT TCATCCTGGC CCTCCACAGG
 16101 AAGATCAAGA ATGAGCCCCG GGTGTTCTC GAGGGGTGAG TTGTCACCCC
 16151 AGGGAAACAA GGGGCTTAC ACCCCTCCTC GGTGCTGAG TTTAGCAGA
 16201 GCTTTGCCC TCTGAGGACC CCACCCAGC CTGCAGATA GAAGGTGGCG
 16251 GTGCTGTTCC CTGGGAGGG CCCCTGAATA GATGGACGGG AGGGACTCTG
 16301 GAGCCAAGGG TCTCCGCAAC GTCACTGTGT GGATGGGAAC CCTGAGATCC
 16351 AGGGTTGGCC AGGGATGACC ACAGGCATCA TTCACACCA TCCTTCACCG
 16401 CAGGCCCTGCC TGGGGTCAGT GGCGCCAGCC CCACCCAGCC CCTGACTCA
 16451 AGGGAAACTT CTCCCTCCCC CACTCAGGGT CAGGGAACTT CAAGATGCCA
 16501 GTGCGTGCTC CCCATTAC AGATGGAAAA GAGGATGCTC TGGAGGAGAG
 16551 CGGTCAAGGG GCTGGGACTC AAGCCACTCT TCCTCCCCAC TCTTCCATT
 16601 GTGACCGAGG TCTCTGAGCG TAGCAGGGAT GTGGGGGAGG CCTCTTGCTC
 16651 ATGCATGGTT CGCTCTATGA CGGCCACCGT GGCAAGCCACA GCCTGAGCTC
 16701 CCAGGCTCCT CTTTCAGCA GTGGATTTCAGA GGAGTGAAT GGAGGCCGGG
 16751 TGCGGTGGCT CACGCCGTGA ATCCCAGCAC TTTGGGAGGC TGAGGTGGGC
 16801 AGATCACCTG AGTTAGGAGT TAGAGACCAG CCTGGCCAAC ATGGTGAAAC
 16851 CCCATCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGCGCACATC
 16901 TGTAGTCCCA GCTACTCGGG AGGCTGAAGC ACGAGAATTG CTTGAACCCA
 16951 GGAGGCAGAG GTTGCACTGA GCCTGGCGA CAGAGCAAGA CTCTGTCTCA
 17001 AAAAAAAAAAA ACAGAAGAAA GAAACTGAAT AAGGCCGGGT GCGGTGGCTC
 17051 ACACCTGTAA TTCCAGCACT TTGGGAGGCC AAGGAGGGCG GATCACGAGG
 17101 TCAGGAGATC GAGACCATCC TGGCTAACAC GGTGAAACCC CATCTCTACT
 17151 AAAAATAGAA AAAAATTAG CCGGGCGTGG TGGCGGGCGC CTGTAGTCCC
 17201 AGCTACTCGA GAGGCTGAGG CAGGAGAACG GCGTGAACCC GGGAGGCAGA
 17251 GTTTCAGTG AGCTGAGACC GTGCTACTGC ACTCCAGCCT GGGCGACAGA
 17301 GCGAGACTCT GTCTCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 17351 AACAAAAAAC AACAAACAAA AAAAGAAAAT GAAACGGGAC TTGTAACAG
 17401 CGACTCCTGC TCTCTCTGC TTATTCCTG TGTTGGCCCC AAGCCCTGCT
 17451 GAGCCCTCTT CTTCCCTGTC TCTGGGCCCTT GTTGCCACTT ATACCCCTTG
 17501 CCTCATTAG GCCTCAGGCC CCTCCCCAGA CTTATCTAGC CACCTTCCCC
 17551 CTGGTCTCGC TGCTGCTGGC CTCCCTCCAG TCCAGCCAAC ACATTCAAGGC
 17601 GGGGACAGCC CTGATAAAAGC ACAACAAATC TGCCCTGCATC TCTTGCTGA
 17651 AGTTTGTCTG AAGCTTCTCA AAGCCACACC CTGGCGCTAG CATTACACG

FIGURE 3F

17701 TCTCCGGGTT CTGCCACCG CTCGCTCTGG GCGGCCTCAC TCCCTTCCCC
 17751 GAGCACCAGC CAGCTGGCT CTGTCCATT CCTCCCATC CTGTGGTTGC
 17801 CTTCCCTCCC TGCCCTCCACA GTTGTACCCC TGGTGCCTCT CTTCCGTCTA
 17851 TACCCCCCTGC TGAGGGGTGT CTTCCTCCCTC AGCCCAGGAA TTTTAAAAGG
 17901 GATGAAGCAT CTAAGACAAC AGGGGAACC GAAGTCAACA GTCCCTGAGAG
 17951 TGGCTTCTG CTCCCTACTC TTGGAAGGAT GGGCTCCCCA AGACCACTGG
 18001 TGGCAAAGAA ACCTGGGTT TGGCCGGCG TGTTGGCTCA CGCCTGTAAT
 18051 CCCAGCACTT TGGGAGGCCA AGGCAGGCCG ATCATGAGAT CAGGAGATCG
 18101 AGATCATCCT GGCTAACACG GTGAAACCCC GTCTCTACTA AAAATACAAA
 18151 AAATTAGCGG GGCACGGTGG CGGGCACCTG TAGTCCCAGC TACTCGGGAG
 18201 GCTGAGGCAG GAGAATGGCA TGAACTGGG AGGGGGAGCT TGCAGTGAGC
 18251 CGAGATTGCG CCACTGCACT CCAGCCTGGG CCACAGAGCG AGACTCCATC
 18301 TCAAAAAAAA AAAAGAACCC TGGGGTTTGG GCAGAGAGAG TTGGAGCTGA
 18351 TGTGGCGCTG AGGGGGCTGC TCCCTCCAT CTGAGTCTCC CATCTCTGCC
 18401 TGCACTCTTC TGCTGGCAC TGTGCCAGCC TGCTAACCTC CCTGGGCCCTC
 18451 AGTTTCTCC TCTGTCAAAT GAGAGAGGAT CTTCCTGGG TGTAGAAAAG
 18501 GACGAGGTGG TGAGTGGTC TGAAAGCCTC TGTTGTCCCA TAAAGCGACT
 18551 CTCCCTACCA TCTTGCAC CCATTGGGGT GTCCAGCACCATGAAACTC
 18601 TGTCTGTGCC TCTGTCTGG AGGGAGACTT GACCTCCCTGC TCAGGAAAGG
 18651 CTCTCCAAGC CCTTGTGGT AAATTCCCTGC CTGCTGTCCG GAACTCAGTC
 18701 TTCCCATCCG AGGGACGAAG GTTTCGGGAA GAGAGGTGGA CAGGAAGGGG
 18751 TCCTCATCAG CGGTCCCACC CTCCCCTCCT TCCTTCGCCC TCTCCAGGCC
 18801 AGAAATCAGC GAGGAGCTA AGGACCTGTAT CCTGAAGATG TTAGACAAGA
 18851 ATCCCAGAC GAGAATTGGG GTGCCAGACA TCAAGGTCGG GGAACCTGGGG
 18901 GTCTTGGGCT GGGCTGGGAC ACAGAAAAACA GGAGTCACCT TCCCCTTCTG
 18951 GAGGGATCAA CACAGGATG CATGTGTGTT GGGTTTGAGT CTGTGGACTT
 19001 TGGACCCCTC CAGGTGATT TGTTAATGGC CTGACCTCTC CCCCTCTCCC
 19051 TGCCCTCCCCG GCCCCGACAG TTGACCCCTT GGGTGACCAA GAACGGGGAG
 19101 GAGCCCCCTTC CTCGGAGGA GGAGCACTGC AGCGTGGTGG AGGTGACAGA
 19151 GGAGGAGGTT AAGAACTCAG TCAGGCTCAT CCCCAGCTGG ACCACGGTGG
 19201 TAAGAGAGCC GGGGTAGATG CTCCCTTGTC CTGGAGGGCC TGGGGGACCT
 19251 GAGCCTTGCT CTGTGCCTGG CTCCCCTGGGG GGACAGAGGC CTGCTGGCC
 19301 AGCCAGCTGT GATCCCTGGC CACTGGAGCC GCCATTCTGC TGGAGGCCA
 19351 TGGAGAGGGA GGTCTTGTT CGGGAGACC AGGAGGCTTG GTGAGGAGAG
 19401 TGACTGATTT AAAGAAATAG CGGGCGTGGG GCCGGGCGCG GTGGCTCACG
 19451 CCTGTAATCC CAGCACTTGG GGAGGCCAAG GCGGGCAGAT CACGAGGTCA
 19501 GGAGATCGAG ACCATCCTTG AAACCCGAC TCTACTAAA ATATAGAAA
 19551 TTAGCTGGGC GTGGTGGCG GCGCGTGTAG TCCCAGCTAC TCGGGAGGCT
 19601 GAGGCAGGAG AATGGTGTA ACCCGGGAGG TGGAGTTTG CGTGAGCCGA
 19651 GATCGCGCCA CTGCACTCCA GCCTGGGCCA CAGAGCGAGA CTGGCTCTCA
 19701 TAAAAAAAAAA AAGAAGAAAA GAAAAGAAAG AAATACCGG CGCGGTGGCT
 19751 CACCCCTGGA ATCCCAGAC TTTGGGAGGC CGAGGCGGGT GGATCACGAG
 19801 GTCAGGAGAT CGAGACCATC CTGGCTAATA CGGCGAAACC CCACCTCTAC
 19851 TAAAAAATACA AAAAAATTAG CGGGCGCAG TGGTGGGCAC CTGTAGTCCC
 19901 AGCTACTGGG GAGGCCGAGG CAGGAGAAC GCTTGAACCT GGGAGGTGGA
 19951 GGTGTTAGTG AGCCAAGATC ACGCCATTGC ACTCCAGCCT GGTTGACAGA
 20001 ACGAGACTCC ATCTCAAAAA AAAAAAGAAA GAAATAGATG GCCCTTGCTC
 20051 AGCGGCAGCA GTCAACCGTGA CTGGAAAGAAG CATTTCATTC CGTCCAGACCA
 20101 GTTACTGAGC TTCCGTTCTC CAGGCACTGC ACAAGGTGCC GAGGACAAGG
 20151 CAGGGGAACG GCCTGGGCAG CCTTGGATT GGAGGAGTGG CCCCAAAGCC
 20201 CACGTATCAG TTAGGCGGG CCGCGTCTC CCCCAGAGCC CACGTATCAG
 20251 TTAGGCAGCA CCTGCGTCTC CCCCAGAGCC CACATATCAG TTAGACGGCG
 20301 CCTGCTTCTC CCCCAGCGCC CACGTATCAG TTAGACGGCG CCTGCTTCTC
 20351 CCCCAGAGCC CACGTATCAG TTAGACGGCG CCTGCTTCTC CCCCAGATCC
 20401 TGTGTATCAG TTAGACTGCG CCTGCTTCTC CCCCAGAGCC CACGTATCAG
 20451 TTAGACGGCG CCTGTTACTC CCCCAGAGCC CACGTATCAG TTAGACGGCG
 20501 CTTGCTTCTC CCCCAGATCC CGCGTATCAG TTAGACGGGC CTGGCTCTCC
 20551 CCCAGATCCC CGGTATCAGT TAGACGGGC TGCGTCTCCC CCAGAGCCCA
 20601 CGTATCAGTT AGACGGGCCT CGGTCTCCCC CAGAGCCAC GTATCAGTTA

FIGURE 3G

20651 GACGGCGCCT GCTTCTCCCC CAGAGCCAC GTATCAGTTA GACGGGCCTG
 20701 CGCTCTCCCC AGAGCCCACG TATCAGTTAG ACGGGCGCCTG CTTCTCCCC
 20751 AGAGCCCGCG TATCAGTTAG ACGGGCGCCTG CATCTCCCC GTGCCAACGT
 20801 ATCAGTTAGA CGGCGCCTGC TTCTCCCCCA GAGGCCACGT ATCAGTTAGA
 20851 CGGCGCCTGCG TCTCCCCAG ATCCTGCGTA TCCATTAGAC AGTGCCTGTG
 20901 TCTCCCCTAG TGCCCGCTCA CATTTCGGTT TTGCTCCCT TCCCTGCTC
 20951 AGCTCTGTG TTGGCACTTG GAAAGTGATT CACATAGTCC CCCGTGGCCA
 21001 CCTGGGGCCA CTGAGAGCCC TGCCCTGCC CTGCGTACA GTCAAGTGAG
 21051 TCAGGGCAAG CACAAGGCCA GGAGGAGAGC CAGGGCCACT GCCGTTGGCG
 21101 GGGCGTGGCC TTGCACTTTA TCCCCCTCTG CAGGGTCCC GCCCAGCTGG
 21151 GACCAGCTGG CTCAACTCCT GCCCCCTATG CTTACTTGAC TCTGTGGGGT
 21201 CGCTGGAACC AGGCAACTCC CACGGGGTCC CCATGACAC TTGCGTGTAC
 21251 TTAGGCCACCA TCTCCTCTCT CTCAGACAC TGGAACAACC TCCCACGCTG
 21301 TCCCTTGCTT CTACTCTCAC TCCCTGTCCC CCTGGTCAAT GCTCAACTCA
 21351 GCACCCAGCA TGGTCCCAGT GGCATGAGTG TGTCAACCTCC CAGCTCAGAG
 21401 CCTGCTTCTC ACTCGGGCTG CTGTGTCCCT CAGAACATCGA CCTCCAGCCT
 21451 GTGCCCGCACC ACCCGCCCTG TTTTCTGCG GGGCTCGTGC ACCGTCCCAC
 21501 CATCATGCAC TCGTCTCTGG CCACGTGCCA TGGAAGGGGC TGCCCCAGAG
 21551 CCTTCAGACT TCGCTTCCT CTGCCCCGGGG AGTCCCACCC CCGATGGCCA
 21601 CGGGACTCGC TCCCTCACT CCTTCGGCTT TTTACGCCAG GGTCCCCCTCC
 21651 TAGAGAGAAG CGAGCCTTCC CTGACCCCTGT AGCTTCAGCC TCCCCCTGCTT
 21701 CACACCTCAT CGCCATTCCC TTGTTTTATT TTTTCTTTTC CACTTACTGA
 21751 CATAACATAAT TTACTGATTT TTCTTCTTTA CTTATCGCT GTCTCCCCA
 21801 ACTAGAAATAT AAGCTGTATG ATGGCTGGGC GCAGTGGCTC ACGCCTGTAA
 21851 TCCCAGCACT TTGGGAGGCC AAGGGGGAG GATCACTTGA GGTCAAGGAGT
 21901 TTGAGACCAG CCTGGCAAC ATGCTGAAGC CCCGTCTCTT CTAAAAATAC
 21951 AAAAAAATTAG CCGGGTGTGG TGGTGGACGC CTGTAATCCC AGCTATTAG
 22001 GAGACTGAGG CGGAAGGATC ATTTGAAGCG GGGAGGCAGA GGTTGCAGTG
 22051 AGCCGAGATT GTGCCACTGC ACTCCAGCCC TGGGCAACAA GAGCAAAACT
 22101 CCGTCTGAAA AAAAAGG CTATATGAGG GCAGGAATTG TGGCCTCAGT
 22151 GTGCCCGCAG GGCCTAGAGT AGTGGCCAGC ACCCAGTAGG CAGCCAGTGG
 22201 TGACCGAGTGT TGACGGGATG GATGGACACA AGCGAGGGAG TGAAGGGACT
 22251 GGCAAGTGTG CCGCTGCCCT TCTGCATGCG TGTGAGTCGG CGTGTCTGTG
 22301 GGCAACGGCAT GGAACCGTCC TTGTACCGGA GGAGGGACAA AGGCAGAGAG
 22351 CCAGGCTGCG GCAGCTGTT CCCTCCTGGC AGCCCCACTG ACTGGGCCAC
 22401 CGGCTGCGGC TCAGCCGTT CCCGGGCCGC CCTGCAGTAG CATCTGGCA
 22451 TCTTCTCGGC GGCCCGAAGG CGGGAGGAT GGCACAGCAT CCCTCCATGG
 22501 CATTGCTGCC GTAGCGAGAA GGTATCTTCT AATGGACTCC CACTTCCAGC
 22551 CCTGGCCCTC CCCACTCTTT CAGCCTGGCC TTGGGGACCC TTCATGGCT
 22601 GGTCCCGGCC CCCTCCCTCAT GTACCACTGG CATCCGGCTC CTCACCATT
 22651 CAGGAATATG CCCCCAGCTG CCAGCGCCCC GTGTTCTTGC CTCTGCCATT
 22701 TCATGCTGTG CTGATTGAGA TGGGACCCGC ACTGCGGCC CTTGGCAGC
 22751 TGCTCTCGGG GAATCGGAGC AGAGGCTGCG TGTCTGGGAG CCTGGGACCT
 22801 GTGCTCTCA CGCTGCCTTG TCCTCCTCA GATCCTGGTGA AGTCCATGCT
 22851 GAGGAAGCGT TCCTTGGGA ACCCGTTGA GCCCCAAGCA CGGAGGGAAAG
 22901 AGCGATCCAT GTCTGCTCCA GGAAACCTAC TGGTGTAAAGT ACTGGTGGGC
 22951 CAGGGACTGC CGGGCACTCC CTGGAGTTGG GTGGGGAGGT CTGAGGCCCA
 23001 TCCTCCACT CTCACGTGCG TTGGGCAAG GCCAGAGCCT GGGGACTTGG
 23051 CCAGGTCTCG GTGTTGGCC CATTGCACT TCTGTCCCCA AGGTTAGTCG
 23101 GGGCTAGAAG GGACCTTTTG GGCCCAGCTC TTGCTTCATT CCTGGGGCCA
 23151 GCATCCCTCA CACACACACT TCCAGGGATG AGGAGCTCAC GCAGCCCCCTC
 23201 CATGGGACAG GAAGACCCCTT CTTCCATGCA GCTTGATGTC ACTCTCTCAC
 23251 TGGGTCCAGC CCCCCTGGGG CTTCAAATCT GTGGCCCCCT CAGCCCTTGG
 23301 CAGCCTGGCA GAGGTTTGC A GACAGGCTGA TGTGGCTTC CTGAGGAGG
 23351 CTGGCGGGCT GTAGAGGAGG GGTGCTGGCC CCTCTGCCCTG GCCCTGGGA
 23401 CTGTTGGCTG CTCTCCCAAG TGGGCCAGGC TGCGTGCAGC CATTGCTGGG
 23451 GCTCTGTGCC CAGTCAGCAC TTTGTGAGTG CTTGTTCACT GAGTAAGCAG
 23501 GGACAGGCTG GCCGGTGAC CACGGGAGAG GAACCCGCA TGGCCGAGGG
 23551 CTCCCTATGG TGAGCCACGC CTGTTGGTTC ACCACCTCCT AGGAGGGTCC

FIGURE 3H

23601 AGAAAAGCAG CTCCCCAAGC CTGTGCGCCT CGTCCTCAGC AGATCCACCT
 23651 TCTTCACTAT AATAAAAGCC AGTCTGGAT GCTAATAAGG CCTGTGCTGG
 23701 AGTTTGACA CAAACCTGCA GAGAGAAAAC CAGTGGGTC CTGAACCACA
 23751 GCGTGGTCCT GGGACAGCCA CTGCCTTCCT CTGGCCCCGG AGGGAAAGCTT
 23801 TGGGAAGGG GCTGGTGGG GTTGTGTTGCC CCACCCCTGGC CTGCTCTGTG
 23851 TGGAAAGGGC ACTCCCCAGA GGGGTGAGTG CCAGGCGCTG TCCGGGTGCC
 23901 TTGGCTTCAC GCTGTCACCA GGCCTGTCGG GGACCACCAT GTTGGTTCC
 23951 CGTAGGCT CCCCTCTATA AGAGGGCCCT TCAGAAGGGT CGGGACCCCT
 24001 CGTAGTGGAC AAGCTGACAT CTGCTCCCTG CTGGAGGTGG CTTGCACCCA
 24051 GGGGAGAGCCT CATAATGAGG TGgggggCCT GGGAGAGGCC TGGAGGTCCC
 24101 AACTGCAGCT TTTCTGTCAT CTCTTCAGGG AGGTGGTTGC GTTGGGGGA
 24151 GGATTCTCTG AGCTCATCCA GGAATGTAGG CCCCTGATGC TGAATTGTG
 24201 CTTAGTGTAG GGGGAGAGGG GGCATATATA ATTTGACGTC CAAATGGGG
 24251 CATTTTGAG AGTGAAGGG GAAGCCATTA ATAATTATGC CAGCACGGCC
 24301 GGGTGCAGGTG GCTCACGCT GTAATCCCAG CACTTTGGGA GGCGGAGGCT
 24351 GGTGGATCAC AGGGTCAGGA GATCGAGACC ATCCTGGCTA ACACGGTGAA
 24401 ACCCGTCTC TACTAAAAAT ACAAAAATAC AGCTGGGCGT GGTGGCGGGC
 24451 ACCTGGAGTC CCAGCTACTC AGGAGGCTGA GGCAGGAGAA TGGCGTGAAC
 24501 CCGGGAGGCA GAGCTTGAG TGAGGCCAAGG TCACGCCACT GCACTCCAGC
 24551 CTGGCGACA GAGTGGAGACT CCGTCTCAA AAATAATAAT TATTATGCCA
 24601 GCATGGTGGC TCATGCCAT AATCCCAGCA CTTTGGGAGG CCAAGGCAGG
 24651 ATTGCTTGAG GCCAGGAGTT CAAGACCAGC CTGGGCAACA TAGCAAGACC
 24701 CCATCTCTAA AAAAAAAAAA AATTAGCCGG GCGTGGTGGT GGGTGCCTGT
 24751 AGTCCCAGCA ACTCAGGAGG CTGAGGTTGGG AGGATTGCTT GAGTCTGGGA
 24801 GGTGGAGGTT GCAGTGAGCT GAGATTGAC CACTGTACTC CAGCTGGGT
 24851 GACAGAGCCA GACCTGTCT CAAAAAAA AAAGAAAAAA AAGTAATAAT
 24901 AATTATGCCA GGACAGCAGG TGGACGGACA CCTGGTCCTT CTGACTCAGA
 24951 GCCTGGTC GCAGCACCCCC TAGTGGTGG ACAAGCCAGA CACAGGATAA
 25001 GGATACATT AGTGTCTAGT TTGACCTGG CAAACAGAGT GACAAGATTG
 25051 GGCTTAATAC TTTCAGCTA TAAAATTCTA GAATTCTGTG ACCCAAGTTT
 25101 AATTGGGGT AGAGCTTTT AAAAAAAA TAGAGATGGA GTCTTGCCAT
 25151 GTGCCAGG CTGGACTTAA ACTCCTGGCC TCAAGCCATT TGCCCACCTT
 25201 GGCTCCGAA AGTGCAGGT GATTACAGGC ATGAGCCACC ACACCCAGCC
 25251 TCCACGTTA ACTTTGAAAG AAGATTTAC TTTCATCATCA AGTCCAATA
 25301 TTATCCTTG ATAGACTGCT TTGGTTTTT GTTTGTTTGT TTTGAGATGG
 25351 AGTTTCACTC TTGTTGCCA GGCTGGAGTG CAGTGGCGCA AACTCAACTC
 25401 ACTGCAGTCT CCGCCTCTCA CATTCAAGCA GTTCTCTTC CTCAGCCTCC
 25451 CAAGTAGCTG GGATTACAGG TGATGCCAC CACCACACCG GCTAATTTT
 25501 GTATTTTAT TAGAGACGGG ATTTCACCAT TTGGCCAGG CTGGTCTCAA
 25551 ACTCCTGACC TCAGGTAAATC TGCCCACCTC AGCCTCCCAA AGTGTGGGA
 25601 TTACAGGCGT GAGCCACTGT GCCCGGCCAT AGAGTTTTT ATACTTTGGG
 25651 ATAATTGTAG AACTCAGTA GTAGAGTTAA GTGGAGTTGG TCCTTTTAA
 25701 AGATATCAA ACCCATTCTAC TGTTTATTTT AAAAAGAGAC ATTTTGGGAG
 25751 GAAAAGTAGA TATAGAAATC TGTTGAATAT GTGACAGAAAT CCCAAGACTG
 25801 ATAGATGGAC TCTGCCCTGT GAACAAGCA AAGAAAAATG CAAATGAAA
 25851 GCCTCTCTAC CCAGATCTGC TGGGGATGA CTGAGGTCAA CACAGAAGGC
 25901 CCTCAGGCCG GGCACGGTGG CTCACGCCCTG CAATCCCAAC ACTTTAGGAG
 25951 GCTGAGGTGG ATGGATCGCT TGAGCCCAAG AGTTTGAGAC CAGCCTGGGC
 26001 AACATGGTGA AACCTGTCTT TTATAGAGAT AAAAAAATAC AAAAATTAGC
 26051 TGGCGTGGT GGCGATGTGCC TGTAGTCTCA GCTACTCAGG AGGCTGAGGT
 26101 GGGAGGATCG CTTGAGCCTG GAAGGCAGAG GTTGCAATGA GCTGAGATTG
 26151 CACCACTGCA CTGCAGCCTG CACGACAGAG CGAGACGCTG TCTCAAAACA
 26201 ACAACAAAAC CACACACACA GAGAGAAGGC CCTTGATTAG GCTGATAGTT
 26251 GGAGGATGTA GGGAAAGTCAG CTGGGTCAAGA CTGTGAGCAG CTCCAGAGGC
 26301 CGTGCTGGGA GTTTAGACT TCATCTCTGG TCAATGGGGG GCCACGGAGG
 26351 CGTTGCGGGC TGAGACTGGG GGCTGAGAGA CCGGCAAGGA GCAACTGCCG
 26401 TGATGTAGGG AGGCCAGAGG GAGGCCAAGC TTGGGGCAAGT GGGTGAAGGG
 26451 GGCTTGAGA GATGTGGGAT TCAGATTCT GTGTGTGTGA GGGAGAGTGT
 26501 CTCCCTGAGT GCATATTCTG ACCCTGAGGT CCCTCTGTCC CTGGTGTCCC

FIGURE 3I

26551 CTGAACAGGA AAGAAGGGTT TGGTGAAGGG GGCAAGAGCC CAGAGCTCCC
 26601 CGCGGTCCAG GAAGACGAGG CTGCATCCTG AGCCCCCTGCA TGCAACCCAGG
 26651 GCCACCCGGC AGCACACTCA TCCCAGGCCT CCAGAGGCC ACCCCCTCAT
 26701 GCAACAGCGG CCCCCCGCAGG CAGGGGGCTG GGGACTGCAG CCCCACCTCCC
 26751 GCCCCTCCCC CATCGTGTG CATGACCTCC ACGCACGAC GTCCAGGGAC
 26801 AGACTGGAAT GTATGTCATT TGGGGTCTTG GGGGCAGGGC TCCCACGAGG
 26851 CCATCCTCCT CTTCTTGAC CTCCCTGGCC TGACCCATTG TGTGGGAAA
 26901 CCGGGTGCCT ATGGAGCTC AGAAATGCCA CCCGGCTGGT TGGCATGGCC
 26951 TGGGGCAGGA GGCAGAGGCA GGAGACCAAG ATGGCAGGTG GAGGCCAGGC
 27001 TTACCACAAC GGAAGAGACC TCCCAGCTGG GCGGGGAGG CCTGGCTCAG
 27051 CTGCCACAGG CATATGGTGG AGAGGGGGT ACCCTGCCA CCTTGGGGTG
 27101 GTGGCACAGG AGCTCTTGT TATTCAAGACG CTGGTATGGG GGCTCGGACC
 27151 CCTCACTGGG GACAGGGCCA GTGTTGGAGA ATTCTGATTC CTTTTTGTT
 27201 GTCTTTACT TTTGTTTTA ACCTGGGGT TCAGGGGAGAG GCCCTGCTTG
 27251 GGAACATCTC ACGAGCTTTC CTACATCTTC CGTGGTTCCC AGCACAGGCC
 27301 AAGATTATTT GGCAGCCAAG TGATGGAAC TAACCTTCCT GGACTGTGTT
 27351 TCGCATTCTGG CGTTATCTGG AAAGTGGACT GAACGGAATC AAGCTCTGAG
 27401 CAGAGGCCTG AAGCGGAAGC ACCACATCGT CCCTGCCAT CTCACTCTCT
 27451 CCCTTGATGA TGCCCCCTAGA GCTGAGGCTG GAGAAGACAC CAGGGCTGAC
 27501 TTTGACCGAG GGCCATGGAC GCGACAGGCC TGTTGGCCCTG CGCATGCTGA
 27551 AATAACTGGA ACCCAGCTC TCCTCTTACA CGGGCTTACCC CATCTGGGCC
 27601 CAAGAGCTGC ACTCACACTC CTACAACGAA GGACAAACTG TCCAGGTGG
 27651 AGGGATCACG AGACACAGAA CCTGGAGGGG TGTCACGCT GGCAGGTGGC
 27701 CTCTGCGGA ATTGCCTCAC CCTGAGGACA TCAGCAGTCA GCCTGCTCAG
 27751 AGGGGGGTG CTGGAGCCG TGAGACACACA GCTCTTCCCG AGCAGCCTTC
 27801 ACCTTCTCTC TGGGATCAGT GTCCGGCTGG CCGACGTGGC ATTTGCTGAC
 27851 CGAATGCTCA TAGAGGTGTA CCCCCACAGG GTCAAGCAGG ACTCGGACAC
 27901 TGCCCTGGAA ACATGGATGG ACAAGGGCTT TTGGCCACAG GTGTGGGTGT
 27951 CCTGTTGGAG GAGGGCTTGT TTGGAGAAGG GAGGGCTGGT GGGGGAGAAA
 28001 CCCGGATCCC GCTGCATCTC CGCGCCTGTG GGTGCATGTC GCGTGCTCAT
 28051 CTGTTGCACA CAGCTCACTC GTATGTCCTG CACTGGTACA TGCACTGT
 28101 ATACAGTTTC TACGTCTATT TAAGGCTAGG AGCCGAATGT GCCCCATTGT
 28151 CAGTGGGTCC ACgtttctcc CGGGCTCCCTC TGGGCTAAGG CAGTGTGGCC
 28201 CGAACGTTAA AAAGTTACTC GGTACTGTTT TTAAGAACAC TTTTATAGAG
 28251 TTAGTGGAAAG GCAAGTTAAAG AGCCAATCAC TGATCCCCAA GTGTTCTTG
 28301 AGCATCTGGT CTGGGGGAC CACTTGATC GGACCCACCC TTGGAAAGCT
 28351 CAGGGTAGG CCCAGGTGGG ATGCTCACCC TGTCACTGAG GGTTTGGTT
 28401 GGCATCGTT TTTTGAATG TAGCACAAGC GATGAGCAA CTCTATAAGA
 28451 GTTTTTAAA AATTAACTTC CCAGGAAGTG AGTTAAAAAC AATAAAAGCC
 28501 CTTTCTTGAG TTAAGGAA AAAAAGGTTTGTCGTA CATTTCCTGC
 28551 ATCTGGATAT ACgtttcttc TCAGCAGCTG GAACAGCTGG CTTTGTGAA
 28601 TTTTCTGGAA GCGTCTGAGG CACCTTAAGT CCCTGAGCAG GACAGTGGTG
 28651 AGAAGTGGTC TTGGCGGAGG GAGGGAGGG GAAGGGCTGG CTCAGGAGGT
 28701 GACCGGGCTG CAGTCCAGGG TACAGCTGAG GCTCCCTGGC GGGTCCGTGG
 28751 CCACTCCTTG GGAAGAACTG CCTGTTTAC AGGGGCTCAG GATGCCAAGG
 28801 TCTGGTCCGG GTAGGAGCA TAGCTGCTGC TTTTGGGCA GAGGTCCCTG
 28851 TGGTGTACA GGAGTGCCTG TGACACCAGC CCAGTGACCT CCCATCCCCG
 28901 CTTAGCCTTG GACACTGGTA CAGACTTTG GGACCCACCA CCTCTGTTC
 28951 CATGGTACAG CCCTCCAGGG CAGCGACGAA AAGAGTCATC CTTAAGGTCA
 29001 CACAGCCCTG AGCTGAATC CAAGCTTGC TACTTTAAAAA TTGTGTGACC
 29051 TTTGGCAGGT CATTGGAGGA GCCTCAGTTC CCTTATTGAT TTAATGGAA
 29101 TGTTCCCGTG GGGTGTTTG TTTGTTGTT TGAGATTTTG TGAGACTTGC
 29151 TCTGTCACCC AGGCTGGAGT GCAATGGCAA GATCTCGGCT CACTGCAACC
 29201 TCTTCCTCCT GGGTTCAAGC GATTCTCCTG CCTCAGGCC CCAAGTAGCT
 29251 GGGACTACAG GTGCCCCGCA CCATGCCCA GCTAATTTTG TGTACTTTA
 29301 GTAGAGACGG GTTTCAACCA TGTTGGCCAG GCTGGTCTTG AACTCCTGAC
 29351 CTCAGGTGAT CTGCCCCACT CGGCCTCCCA AAGTGCTGGG ATTACAGGCG
 29401 TGAGCCACCG CGCCACCTC CCCATGGGT TTGAATGCAA ACAATGCAA
 29451 CGTTTCGTC TGCTCTACA CTACAACAGT GAACACAGAA GACTTCTGTG

FIGURE 3J

29501 ACCGGCTGGG CGCGGTGGCT CACGCCCTGTA ATCCCAGCAC TTTGGGAGGC
 29551 TGAGGAAGGC GGATCATGAG GTCGGAGATC GAGACCATCC TGGCTGACAC
 29601 GGTGAAACCC CGTCTCTACT AAAAATACA (SEQ ID NO:3)

FEATURES:

Start: 3000
 Exon: 3000-3359
 Intron: 3360-4259
 Exon: 4260-4307
 Intron: 4308-4749
 Exon: 4750-4803
 Intron: 4804-5206
 Exon: 5207-5258
 Intron: 5259-5511
 Exon: 5512-5645
 Intron: 5646-6122
 Exon: 6123-6159
 Intron: 6160-7038
 Exon: 7039-7060
 Intron: 7061-8252
 Exon: 8253-8341
 Intron: 8342-12264
 Exon: 12265-12464
 Intron: 12465-15226
 Exon: 15227-15280
 Intron: 15281-16061
 Exon: 16062-16135
 Intron: 16136-18797
 Exon: 18798-18885
 Intron: 18886-19070
 Exon: 19071-19199
 Intron: 19200-22830
 Exon: 22831-22934
 Intron: 22935-26558
 Exon: 26559-26628
 Stop: 26629

CHROMOSOME MAP POSITION:

Bac accession number: AC005940
Chromosome: 17

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
2082	G	A	Beyond ORF(5')			
2748	-	C A	Beyond ORF(5')			
8868	G	A	Intron			
10187	G	A	Intron			
10216	T	C	Intron			
11100	G	A	Intron			
11650	G	A	Intron			
11656	A	C	Intron			
15095	C	T	Intron			
15116	A	G	Intron			
15428	A	G	Intron			
15827	T	C	Intron			
16135	G	A	Exon	375	G	E
16557	A	G	Intron			

FIGURE 3K

17375	C	T G	Intron
17375	G	C	Intron
17375	A	C G	Intron
17375	A	C G	Intron
17511	C	T G	Intron
17928	A	C	Intron
17968	C	G	Intron
18574	T	C	Intron
19654	C	T	Intron
21498	C	T	Intron
22729	G	A	Intron
22757	C	T	Intron
22779	C	T	Intron
24350	T	G	Intron
24558	T	C A	Intron
24872	-	A	Intron
25756	C	T	Intron
25968	G	A	Intron
26537	G	C	Intron
28204	C	T A G	Beyond ORF(3')

Context:

DNA Position	
2082	<pre> ATGCAGAGTCCAGCGCAAGCAGGGGAAGGGCATCAGGTTGGCATGCCAGCGCTAC AAGCCTGGGACAGAGATGGGGCTCTAGGTGAGTGTCAAGGGTCAGTCGGGGTCAGGA TGTAGCCCAGGGTCATGGCTGAAGGTGAGGGCTGGGGTCACCTCCCTGATGTTTCAGCC GCCACACAGTGAGTTGAGAACATGAGTCTCAGGGATGTCATGCCCTGTTTACCCCT CATTCCCTCATCCCCATCCCTTGCTTTTTTGAAACCGAGTCTGCTCCATCACCCA [G,A] GCTGGAGTGAGTGGCGTGATCTGGCTACTGCAACCTCCACCTCCAAAGTTCACACGA TTCTCTGCTCAGCCTCCCGAGTAGATGGGATTTCAAGGTGACGCCACATGCCCTGGCT AATTTTTGATTTTAATAGAGACAGAGTTTGCCATGTTAGCCAGGCTAGTCTCGAACT TCTGACCTCAGGTGATCCACCTGCCCTGGCTCCCAAAGTGCTGGATTACAAGTGAG CCACCATGTTGGGCCATCCCTGTTGACAGACGTCAATGAGGCAAGGCTGGCTGGA </pre>
2748	<pre> CAAGGAGGGCTCCCTGGAGGAGGCAGGTGGCTGAAGCATCAGCAAGGCTCTGAGTTA CTAGTGTCTAGCTCAGCTCCAGGAGGCAGTGTCTGGAGTGCTGTCAGGTTGG ACTCATGACTCACAGGGCTGCATGCTGTCTGGCTGAGCTGACCCCTGGCTGCCCC TTCCAGTGTGCTGGGCTCCAGGCTTCTGCCCTGTCGCTGATTCCAGAATATCAGA TTCTCTGCTTCCCTGTGAAGCCAGCAGGCAAGTGACTGCCTCTGTTACCGCAGGG [-,C,A] TACTGAGGCCTAGAGGGCTGGCATGCCAGAACCGATGTAATTCACTCAGGTCAAGG GACAGACTTGAGTTGGGTGTTGCAATCCGGTAGAGGAAACGCCAGGGCAAAGGCAT GGAGGTGGGACCCACAGCGCTGTGGTACCTTACCTGTTAGCCAGCCTGACACCCAGGAG TGAAGCCTTCTCTGCCCTCTTCTCAGGTTCCAAACAGGTAACGCGAGAAGAACCCCT TGACTGAAGCAATGGAGGGGGGTCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGG </pre>
8868	<pre> TCCTGTGGGTCTGAGTCTGGCTTCTGTATCTTCTGCTGAGTTCTAGCCTAGC TTAGCGTTGCCACGGGGCTTCAAGAGATGTGGGAAGGAAGGGATTTATGTCAGCTGCTG GGGAGAGTCTGCTCTGGCATGGGGCGGGCATGGTGGCAGGGTGGATTTACCTGTGAGG GGCCCTAGTCTGATAAGAGCTCAGGAGGGTGTAGTGAGCTGGCCTCTGTCATTTCAT TCATTAGCTACATTCACTGCCCTGGGGCATAGGGTGAAAGACCCAGACCCAGTTCAC [G,A] GCCTAGTGGGAGGGACAGGAATCTAGGCAGGGCAGATAATACAGGGTGGCTGCCAAGG CTGGGGAGCCTAGAGGCTGTAGGAGTGCCGGGGCTGGGGAGTCTCCCTGAAGAGGCT ACTTATGATTGGGTCTGAGGGATGAGTAGACTCCCTGCTCAGGTTTGAGGGATGGG CGTGGAAAGACGATGTGCCCTGGCATAGGCAGTGTACTCTGAGTCTGGGGAGAAGTGGAGTCT </pre>

FIGURE 3L

	GGCTGAAGCCTCCAGTGGCAGAGGAGGCCGTGGTAGTGAAAGATGATGCTGAAACA
10187	TTCCCTGGGGAACAGGGTGGGATCTGGCTGAGGTTGACCTGCAGTGACAGAAACAGG ACTGTCTTATCCTGCTCGAGCCTCTCCTTGCCTCAGATTAAGACTCTTTGCACAT ATGGGAAACTGAGGCACACAGAGGGAGGGCTTGAGAAAATCCCTACCAAGGGCTA GAGGCATGGATGGAAGGGACATTACCCGGTACGGTCAGTGGCAGGCAC [G,A] GTCCTGTACCAAGCTGGCTCACCTCCTTCTGTTGAGTCCCTCTTCCCCTGAAGTC CTGTTGCTGATCCCCTAGCCTCACAAAGAAACGAGTTATCTTACCTGGTCTTGG GTAAAGCCTCATCAGGACCCAGCTAATCACAGTGAAGGGCTCCCTGGGGAGAACCGTT AGCGCCAGGGCTGACAGGTGGATGAACAGAGGCACAGGGCGTGAAGACCTGCCTTG TGATTCTGGCCCCAAGAAGAGAGTTGAGGCTGCCATGAGAGGGCTGGTGGTCAGGGC
10216	TTCCCTGGGGAACAGGGTGGGATCTGGCTGAGGTTGACCTGCAGTGACAGAAACAGG ACTGTCTTATCCTGCTCGAGCCTCTCCTTGCCTCAGATTAAGACTCTTTGCACAT ATGGGAAACTGAGGCACACAGAGGGAGGGCTTGAGAAAATCCCTACCAAGGGCTA GAGGCATGGATGGAAGGGACATTACCCGGTACGGTCAGTGGCAGGCACAGTCCT GTACCAGCTGGCTCACCTCCT [T,C] TCTGTTGAGTCCCTCTTCCCCCTGAAGTCCTGTTGCTGATCCCCTAGCCTCCACA AAGAAACGAGTTATCTTACCTGGTCTTGGTAAAGCCTCATCAGGACCCAGCTAATCA CAGTGAAGGGCTCCCTGGGGAGAACCGTTAGCGCCAGGGCTGGACAGGTGGATGAAC AGAGGCACGAGGGCGTGAAGACCTGCCTTGATTCGGCCCCAAGAAGAGAGAGTTGA GGCTGCCATGAGAGGGCTGGTGGTCAAGGGCCAGGCTGGTCTCAGTTGATGGGG
11100	ATCGATGCCCTAGCTGCCAGTTATCTACCAAGATGTCATTGGAAATCTATGTGGTAA GAGCTGGAGTTCAAGGGAGAGGCTAGGGTTTGAGATAAGAACATGAGACCCTTCCATG GTCAAATGTCACCCCCCTGAGCTTCTGCCCCCTGAAGGGTGTGTCAGATTCTTGTG TGCCTGGCACATAGTAGGCAATCAAGAAAGTCCACTGGTTATGGTTATTGTTATAAG GCACCCGCCCTCTGCCCCAGCCTCCCTCTCCCTCTCCCTCTCCCTCTTCTCTC [G,A] CCTTCTCTCCCTCTCCCTCCAGCATCTGGGTCCGGTGGTCCAGATGAAGGTACTTG CCAAGGAGGGAGCCACAGGTGATGGTGGCTGGGATGGGTCAGTGGGTCATTGTCT CTTGGCTGGGACCTTACCAAGTCATGTCAGTTGAGCACCTGTCACCTGTGGTGGT GGGCCAGAAAGCAGGGCAGACCTCCAGCTTAAAGGTCATTCTGATTTGGGATTGTC CTACTATATGTGGCTGACCTTACACCCAGCTGTGTCATCTGCTTGTCCCAAGGCC TGGGTGCCATC CATCTCTGAAACCCATCAGGCCAGATCCGAGGGCTGAGATGGTACCTCTGAGGAT AGCAGAGTCCCTACAATCTTACTCTCAGTCCAGCAGCAGCAGGACATCTTGCC GGTGGGGATGGAACCTGGAGAAAGGTTTGATGGCTTGGGCTGCAGACGGCACTCAC AGGGAAAGGGCAGAGCTAGCCTAGGAAGAACTCTGCTCCAGCTGGGGCGGTGGCTCAC [G,A] CCTGTAATCCCAGCACTTGGGAGGCCAGGGTGGGTTGACCTGAGGTCAAGGAGTTCA AGACCAAGCTGACCAACATGGCGAACCCCTGTCCTACTAAAAATACAAAAGTAGCCGG GGCTGGTGGCAGACACCTGTAATCCCAACTACTCGGGAGGCTGAGGCGAGGAGAATCT GAACCTGGGAGGTGGAGGCTGAGTGGCAGGAGATCACGCCATTGCACTCCAGCCTGGG GACAGAGTGAAGACTCTGTCAAAAAAAAAAAAACAAAAAAACAGCAACA
11650	GTGGCTGACCTTACACCCAGCTGTGTCATCTGCTTGTCCCAAGGCC TGGGTGCCATC CATCTCTGAAACCCATCAGGCCAGATCCGAGGGCTGAGATGGTACCTCTGAGGATAGCAGA GGCAGAGTCCCTACAATCTTACTCTCAGTCCAGCAGCAGGACATCTTGCC GGTGGGGATGGAACCTGGAGAAAGGTTTGATGGCTTGGGCTGCAGACGGCACTCACAGGGAA GGGGCAGAGCTAGCCTAGGAAGAACTCTGCTCCAGCTGGGGCGGTGGCTCACGCC TGT [G,A] CCTGTAATCCCAGCACTTGGGAGGCCAGGGTGGGTTGACCTGAGGTCAAGGAGTTCA AGACCAAGCTGACCAACATGGCGAACCCCTGTCCTACTAAAAATACAAAAGTAGCCGG GGCTGGTGGCAGACACCTGTAATCCCAACTACTCGGGAGGCTGAGGCGAGGAGAATCT GAACCTGGGAGGTGGAGGCTGAGTGGCAGGAGATCACGCCATTGCACTCCAGCCTGGG GACAGAGTGAAGACTCTGTCAAAAAAAAAAAAACAAAAAAACAGCAACA
11656	GACCTTACACCCAGCTGTGTCATCTGCTTGTCCCAAGGCC TGGGTGCCATCC TCTGAAACCCATCAGGCCAGATCCGAGGGCTGAGATGGTACCTCTGAGGATAGCAGA GTCCCTACAATCTTACTCTCAGTCCAGCAGCAGGACATCTTGCC GGATGGAACCTGGAGAAAGGTTTGATGGCTTGGGCTGCAGACGGCACTCACAGGGAA GGGGCAGAGCTAGCCTAGGAAGAACTCTGCTCCAGCTGGGGCGGTGGCTCACGCC TGT [A,C] ATCCCAGCACTTGGGAGGCCAGGGTGGGTTGACCTGAGGTCAAGGAGTTCAAGGACCA GCCTGACCAACATGGCGAACCCCTGTCCTACTAAAAATACAAAAGTAGCCGGCGTGG TGGCAGACACCTGTAATCCCAACTACTCGGGAGGCTGAGGCGAGGAGAATCT CTTGACCT GGGAGGTGGAGGCTGAGTGGCAGGAGATCACGCCATTGCACTCCAGCCTGGGGACAGA

FIGURE 3M

GTGAGACTCTGCTCAAAAAAAAAACCAAAAAAAACAGCAACAACCTCTC
 15095 GGCTGTTGCAATATCAGGAAGAAGGTGGATTATGAGGGAGAAGGGATGACTCCTTGAAGC
 CCGAGCTGGTTAGTGAGCAGAAGTCCATATACCATCATTCTGGGTGCGTCTGTG
 GCACGGGAGCGGCCGTGTGACCCCTCTGGATGAAGGAGGTTTGACCTGTTGAGTTGGA
 AACGTACCTGGTAGAGTCCTTCCAAGGAAACCAGAACCCCTGGAGGGTGGAGGCCTT
 GTTCTGGCGCCCCGTGTCTCAGCACTCAGCACGGGCCAGCATCGGGCAAGTACCG
 [C, T]
 GGAGTGTGTCGAGTGAGTACATGACAGAGGAAAGAGGTTCCCTGCAGGCCTCTCCTGC
 AGCCCGCTGGAGCTGGGTGGCAGAGGTGGCTGTGCCCTGGGGACTGATGTGAGCATG
 TTTCTTCAGGCTTGGATGTATGGGCCACTGGCGTACGTTGACTGCTTTGTCTATG
 GGAAGGTGAGTGCAGGGATGCCAGCAGAGCTGGGGGGGTCCAGTGAGGCGGGCACGGG
 CGACGGATGCAAGCTCTTCTTGTCTTAAGTGGCTTTGAAAGAGCCCACCTGGCT
 15116 GAAGGTGGATTATGAGGAGAAGGGATGACTCCTTGAAGCCCGAGCTGGTTAGTGAGCAG
 AAGTTCCATATATACCATCATTCTGGGTGCGTCTGTGGCACGGGAGCGGCCGTGTGA
 CCCTCTGGATGAAGGAGGTTTGACCTGTTGAGTTGAAACGTACCTGGTTAGAGTCTT
 TCCAAGGAAACCCAGAACCCCTGGAGGGTGGAGGCCTTGTCTGGCGCCCTGTGTCC
 TCAGCACTCAGCACGGGCCAGCATCGGGCAAGTACCGCGGAGTGTTGTCAGTGAGT
 [A, G]
 CATGACAGAGGAAAGAGGTTCCCTGCAGGCCTCTCCTGCAGCCCGCTGGAGCTGGGTGGG
 CAGAGGTTGGCTGTGCCCTGGGGACTGATGTGAGCATGTTCTTCCAGGCCTGGATG
 TATGGGCCACTGGCGTACGTTGACTGCTTGTCTATGGGAAGGTGAGTGCCAGGGATG
 CCAGCAGAGCTGGGGGGTCCAGTGAGGCGGGCACGGCGACGGATGCAAGGCTCTTCT
 TTTGTCTTAAGTGGCTTTGAAAGAGCCCACCTGGCTCAGAGAAGGCTGAGAGAGAAG
 15428 AAAGAGGTTCCCTGCAGGCCTCTCTGCAGCCCGCTGGAGCTGGGTGGCAGAGGTGGCT
 GTGCCCTGGTGGGACTGATGTGAGCATGTTCTTCCAGGCCTGGATGTATGGGCCACT
 GGGCTCACGTTGACTGCTTGTCTATGGGAAGGTGAGTGCCAGGGATGCCAGAGCT
 GGGGGGGGTCCAGTGAGGCGGGCACGGGACGGGATGCAAGGCTCTTCTTGTCTTA
 AGTGGCTTTGAAAGAGCCCACCTGGCTCAGAGAAGGCTGAGAGAGAAGAGGCTTTCT
 [A, G]
 TCTTTCTGGTCCCTGGGGAGCGATTCTCGCGAAGGAGTCGCAGGAACAGCAGACACCT
 AAGGGGAGGTGCCAGCATGGTGTGCCACGCCAGCCAGTGCTCCCCGTCCCTCT
 GTCCCTTGACGCCATTCACTTATTGAGCCATGTGTTCACTCCCTGCTATTATTGAC
 AAATTGTCCTTACCCCTACCCCTGGCTGAGGCTGGACCCCTGGGACACCAACGCTGAGC
 TATCGGTGATCCCTGCCGCAGGTGTGCCCTGGTACCAACTAAGGGCAGGGGG
 15827 CCAGAGTGCTCCCCGCTCCCTGTCCCTGACGCCATTCACTTATTGAGCCATGTGTTCA
 CTCCCTTGCTATTATTGACAAATTGTCCTTACCCCTACCCCTGGCTGAGGCTGGACC
 CTGGGGACACCCAACGCTGACGTATCGGTGATCCCTGCCGCAGGTGTGCCCTGCTGGT
 GACCACACTAAGGGCAGGGGGAAATTTCAGTGAACATGTTCCAAGCCCCAGGCCCTGG
 GAGTGGAGGGCTGGCACAGGTGGCGTAATGGTGGTGGGTGCACCCAGCCTGGCTGGC
 [T, C]
 TGGCGGGGGTGGCAGTAACGGCGGTGGATGCAACCCAGCCTCATTGTTCCCTCAGCAACT
 CATTCAATTGAGTCACATTGTAACATTACAGTGTGAGTTGAGGTCTTCTCATGTA
 ATGGGAGGCCAGACCTGCCCCCTACCCCTGCCCCACCAAGGGAGGGGGGTTGATCCCCT
 GGCACAGGTCGAGGCCCTGGACCCACATCCTTGTCTGCCCTCTCCACCCACAGTGCCCG
 TTCACTGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCGTGGTITT
 16135 GGGTGGCAGTAACGGCGGTGGATGCAACCCAGCCTCATTGTTCCCTCAGCAACTCATTCA
 TCAGTCACATTGTAACATTACAGTGTGAGTTGAGGTCTTCTCATGTAATGGGAG
 CCCAGACCTGCCCCCTACCCCTGCCGCACCAAGGGAGGGGGTTGATCCCCTGGCACAG
 GTCGAGGGCCCTGGACCCACATCCTTGTCTGCCCTCCACCCACAGTGCCCGTTCATCG
 ACGATTCATCCTGCCCTCCACAGGAAGATCAAGAATGAGCCGTGGTGTTCCTGAGG
 [G, A]
 GTGAGTTGTCACCCAGGGGAAACAAGGGGGCTACCAACCCGCTCTGGTGTCTGAGTTTA
 GCAGAGCTTTGCCCTTGAGGACCCCACCCAGCCTGAGATATGAAGGTGGCGGTGCT
 GTTCCCTGGAGGGACCCCTGAATAGATGGACGGGAGGGACTCTGGAGCCAAGGGCTCC

FIGURE 3N

GCAACGTCACTGTGTGGATGGGAACCCCTGAGATCCAGGGTTGCCAGGGATGACCACAGG
 CATCATTACACCAACTCCTCACCGCAGGCCTGCCCTGGGTCACTGGGCCAGCCCCACCC
16557
 TTCCCTGGGAGGGACCCCTGAATAGATGGACGGGAGGGACTCTGGAGCCAAGGGTCTCCG
 CAACGTCACTGTGTGGATGGGAACCCCTGAGATCCAGGGTTGCCAGGGATGACCACAGGC
 ATCATTACACCAACTCCTCACCGCAGGCCTGCCCTGGGTCACTGGGCCAGCCCCACCC
 AGCCCCTGGACTCAAGGGAACTTCTCTTCCCCACTCAGGGTCAGGGAACTTCAAGAT
 GCCAGTGCCTGCTCCCCATTCACAGATGAAAAGAGGATGCTCTGGAGGAGAGCGGTCA
 [A, G]
 GGGGCTGGGACTCAAGCCACTCTCCCTCCCCACTCTTCCATTGTGACCGAGGTCTCTGA
 GCGTAGCAGGGATGTCGGGGAGGCCTTGTCTCATGCATGGTTCGCTCATGACGGCCAC
 CGTGGCAGCCACAGCCTGAGCTCCCAAGGCTCCTTTCACTCAGCAGTGGATTCAGGAGTGA
 AATGGAGGCCGGGTGCGGTGGCTACGCCCTGTAAT
17375
 GAGGCCAAGGGAGGGCGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAACACGGTG
 AAACCCCCTCTACTAAAAATAGAAAAAAAAATTAGCCGGCGTGGTGGCGGGCGCTGT
 AGTCCCAGCTACTCGAGAGGTGACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCT
 TCAGTGAGCTGAGACCGTGTACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCT
 CAAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAA
 [C, T, G]
 AAAATGAAACGGGACTTGTACTCAGCGACTCCTGCTCTCTGCTTATTCTGTGTGG
 TCCCCAAGCCCTGCTGAGCCCTCTTCCCTGTCTCTGGCGTTGCACTTATACC
 CCTTGCCCTATTCAAGGCTCAGGCCCCCTCCCCAGACTTATCTAGCCACCTTCCCCCTGGT
 CTCGCTGCTGCTGGCTCCCTCCAGTCCAGCCAACACATTCAAGGGGGGACAGCCCTGAT
 AAAGCACAACAAATCTGCTGATCTTGCCTGAAGTTGTCTGAAGCTTCTCAAAGCC
17375
 GAGGCCAAGGGAGGGCGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAACACGGTG
 AAACCCCCTCTACTAAAAATAGAAAAAAAAATTAGCCGGCGTGGTGGCGGGCGCTGT
 AGTCCCAGCTACTCGAGAGGTGAGGCAGGAGAACGGCGTGAACCCGGGAGGCAGAGGT
 TCAGTGAGCTGAGACCGTGTACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCT
 CAAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAA
 [G, C]
 AAAATGAAACGGGACTTGTACTCAGCGACTCCTGCTCTCTGCTTATTCTGTGTGG
 TCCCCAAGCCCTGCTGAGCCCTCTTCCCTGTCTCTGGCGTTGCACTTATACC
 CCTTGCCCTATTCAAGGCTCAGGCCCCCTCCCCAGACTTATCTAGCCACCTTCCCCCTGGT
 CTCGCTGCTGCTGGCTCCCTCCAGTCCAGCCAACACATTCAAGGGGGGACAGCCCTGAT
 AAAGCACAACAAATCTGCTGATCTTGCCTGAAGTTGTCTGAAGCTTCTCAAAGCC
17375
 GAGGCCAAGGGAGGGCGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAACACGGTG
 AAACCCCCTCTACTAAAAATAGAAAAAAAAATTAGCCGGCGTGGTGGCGGGCGCTGT
 AGTCCCAGCTACTCGAGAGGTGAGGCAGGAGAACGGCGTGAACCCGGGAGGCAGAGGT
 TCAGTGAGCTGAGACCGTGTACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCT
 CAAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAA
 [A, C, G]
 AAAATGAAACGGGACTTGTACTCAGCGACTCCTGCTCTCTGCTTATTCTGTGTGG
 TCCCCAAGCCCTGCTGAGCCCTCTTCCCTGTCTCTGGCGTTGCACTTATACC
 CCTTGCCCTATTCAAGGCTCAGGCCCCCTCCCCAGACTTATCTAGCCACCTTCCCCCTGGT
 CTCGCTGCTGCTGGCTCCCTCCAGTCCAGCCAACACATTCAAGGGGGGACAGCCCTGAT
 AAAGCACAACAAATCTGCTGATCTTGCCTGAAGTTGTCTGAAGCTTCTCAAAGCC
17375
 GAGGCCAAGGGAGGGCGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAACACGGTG
 AAACCCCCTCTACTAAAAATAGAAAAAAAAATTAGCCGGCGTGGTGGCGGGCGCTGT
 AGTCCCAGCTACTCGAGAGGTGAGGCAGGAGAACGGCGTGAACCCGGGAGGCAGAGGT
 TCAGTGAGCTGAGACCGTGTACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCT
 CAAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAA
 [A, C, G]
 AAAATGAAACGGGACTTGTACTCAGCGACTCCTGCTCTCTGCTTATTCTGTGTGG
 TCCCCAAGCCCTGCTGAGCCCTCTTCCCTGTCTCTGGCGTTGCACTTATACC
 CCTTGCCCTATTCAAGGCTCAGGCCCCCTCCCCAGACTTATCTAGCCACCTTCCCCCTGGT

FIGURE 30

	CTCGCTGCTGCTGGCTCCCTCCAGTCCAGCCAACACATTCAAGGGGGGACAGCCCTGAT AAAGCACAACAAATCTGCCTGCATCTTCGCTGAAGTTGTCTGAAGCTTCTCAAAGCC
17511	GAGGCTGAGGCAGGAGAACGGCGTGAACCCGGGAGGCAGAGGTTCACTGAGCTGAGACC GTGCTACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCTAAAAA AAAAAAAAACAAAAA AAAAAAAAACAAAAA ACAAACAAAAA AGAAAATGAACAGGGAC TTGTA CTAGCAGTCTCTGCTCTCTGCTTATTTCTGTGTGGTCCCCAAGCCCTGCT GAGCCCTCTCTTCCCTGTCTCTGGGCCCTGTGTTGCCACTTACCCCTTGCCATTAG [C, T, G] CCTCAGGCCCCCTCCCCAGACTTATCTAGCACCTTCCCCCTGGTCTGCTGCTGGCC TCCCCTCAGTCCAGCCAACACATTCAAGGGGGACAGCCCTGATAAAAGCACAACAAATCT GCCTGCATCTCTTGCTGAAGTTGTCTGAAGCTTCTCAAAGCCACACCCCTGGCGCTAGC ATTACACAGTCTCCGGGTTCTGCCACCCGCTGTCTGGGGCCCTACTCCCTTCCCG AGCACCAGCCAGCTGGCTCTGTCCATTCTCCTCATCCTGTGGTGTGCCCTCCCTCCCT
17928	ATCTGCCTGCATCTTCGCTGAAGTTGTCTGAAGCTTCTCAAAGCCACACCCCTGGCGC TAGCATTACACGTCCTCGGGTTCTGCCACCCGCTGTCTGGGGCCCTACTCCCTT CCCGAGCACCAAGCCAGCTGGCTCTGTCCATTCTCCTCATCCTGTGGTGTGCCCTCCCT CCCTGCCCTCCACAGTTGTAACCCCTGGTGCTCTCTCTGTCTATACCCCTGCTGAGGG TGTCTTCCCTCAGCCCAGGAATTAAAAGGGATGAAGCATCTAAGACAACAGGGGA [A, C] CCGAAGTCAACAGTCTGAGAGTGGTTCTGCTCCCTACTCTTGAAGGATGGGCTCCC CAAGACCACTGGTGCAAAGAACCTGGGTTGGCCGGCGTGGTGGCTCACGCCGTGA ATCCCAGCACTTGGGAGGCCAGGCAAGGCAGGGGATCATGAGATCAGGAGATCAGGATCATC CTGGCTAACACGGTAAACCCCGTCTCTACTAAAAATACAAAAAATTAGCCGGGACGGT GGCGGGCACCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATGGCATGAACCTG
17968	TCAAAAGCCACACCCCTGGCGCTAGCATTACACGTCTCCGGTTCTGCCACCCGCTCGTCT GGGGCCGCTCACTCCCTTCCCGAGCACCCAGCTGGCTCTGTCCATTCTCCTC ATCCCTGTGGTTGCCCTCCCTCCCTGCTCACAGTTGTAACCCCTGGTGCTCTCTCTG CTATACCCCTGCTGAGGGGTGCTTCCCTCAGCCAGGAATTAAAAGGGATGAAG CATCTAAGACAACAGGGGGAACCGAAGTCAACAGTCTGAGAGTGGTTCTGCTCCCTA [C, G] TCCTTGAAGGATGGCTCCCAAGACCACTGGTGGCAAAGAACCTGGGTTGGCCGGG CGTGGTGGCTACGCCGTGAATCCCAGCACTTGGGAGGCCAGGCAAGGCGGATCATGAG ATCAGGAGATCAGGATCATCTGGCTAACACGGTGAACACCCGCTCTACTAAAAATACA AAAAATTAGCCGGGACGGTGGGGCACCTGTAGTCCCAGCTACTGGGAGGCTGAGGC AGGAGAATGGCATGAACCTGGGAGGCCAGCTTGAGTGAAGCCGAGATTGGCCACTGCA
18574	GCCTGGGCCACAGAGCGAGACTCCATCTCAAAAAAAAAAGAACCCCTGGGTTGGCA GAGAGAGTTGGAGCTGATGTGGCGTGAAGGGGCTGCTCCCTCCATCTGAGCTCCCAT CTCTGCCCTGCACTCTCTGGCTGGCACTGTGCCAGCCTGCTAACCTCCCTGGGCTCAGT TTCCCTCCTGTCAAATGAGAGAGGATCTCTCTGGGTGAGAAAAGGACGAGGTGGTGA GTGGGTCTGAAGGCCCTGGTGTCCCATAAAGCGACTCTCCCTACCATTTGCCACCA [T, C] TGGGGTGTCCAGCACCCATGGAACCTGTCTGTGCCCTGTCTGGAGGGAGACTTGACC TCCGTCTAGGAAAGGCTCTCCAAGCCCTGGTGTGAATTCCTGCCCTGCTGTCGGAAC TCAGTCTCCCATCCGAGGGACGAAGGTTGGGAAGAGAGGTTGACAGGAAGGGTCT CATCAGGGTCCCACCCCTCTCCCTGCCCTCCAGGCCAGAAATCAGCGAGG AGCTCAAGGACCTGATCTGAAGATGTTAGACAAGAATCCCAGACGAGAATTGGGTGC
19654	AGAGGGAGGTCTTGTGGTGGGAGACCAAGAGGGCTTGGTGAGGGAGGTGACTGATTAAA GAAATAGCGGGCGTGGGCGGGCGCGTCAAGCCGTGAATCCCAGCACTTTGGGA GGCCAAGCGGGCAGATCACGAGGTCAGGAGATCAGGACCATCTTGAACCCCCGACTCT ACTAAAAATATAGAAAATTAGCTGGCGTGGTGGCGGGCGCTGTAGTCCCAGCTACTCG GGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGTGGAGTTGCCGTGAGCCGAGAT [C, T] GCGCCACTGCACTCCAGCCTGGGCCACAGAGCGAGACTGCGTCTCAAAAAAAAAAAAAGA AGAAAAGAAAAGAAAGAAATACCGGGCGCGTGGCTACGCCCTGGAATCCCAGCACTTIG

FIGURE 3P

	GGAGGCCGAGGCCGGTGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAATACGGC GAAACCCCACCTCTACTAAAAAATACAAAAAAATTAGCCGGCGCAGTGGTGGGCACCTGT AGTCCCAGCTACTGGGAGGCCAGGCAGGAATCGTTGAACCTGGGAGGTGGAGGTT
21498	GGTCGCTGGAACCAAGGCAACTCCCACGGGTCCCCATGACCACTTGCTGATCTTAGCCA CCATCTCTCTCTCAGACCACTGGAACACCTCCCACGCTGTCCTGCTTCTACTCT CACTCCCTGTCCCCCTGGTCAATGCTCAACTCAGCACCCAGCATGGTCCCAGTGGCATGA GTGTGTACCTCCAGCTCAGAGCCTGCTCTCACTCGGGTGTGTGTCCTCAGAACATC AGACCTCCAGCCTGTGCCACACCCGCCCTGTTTCTGCGGGGCTGTGACCGTCC [C, T] GCCATCATGCACTCGTCTCTGGCCACGTGCCATGGAAGGGCTGGCCAGAGCCTTCAGA CTTCGCTCCCTCTGCCCGGGAGTCCCACCCCCGATGGCACGGACTCGCTCCCTCAC TTCCCTCGGCTTTTACGCCAGGGTCCCCTAGAGAGAACGAGCCCTCCCTGACCC GTAGCTTCAGCCTCCCTGCTTCACACCTCATGCCATTCCCTGTTTATTTTCCCT TCCACTTACTGACATAACATAATTACTGATTTTCTCTTACTTATGCCCTGTCTCCCC
22729	GCCCTGCACTGAGCATCTTGGCATCTTCTCGCGGCCGAAGGGCGGAAGGATGGCACAGC ATCCCTCATGGCATTTGCTGCCGTAGCGAGAAGGTATCTCTAATGGACTCCACTTCCA GCCCTGGCCCTCCCCACTCTTCAGCCTGCCCTGCCGACCCCTCATGGGCTGGTCCCG CCCCCTCTCATGTAACAGTGGCATCCGGCTCTCACCATTCAGGAATATGCCCGCAGC TGCCAGGCCCGTGTCTTGCCCTGCCATTATGCTGTGCTGATTGAGATGGGACCC [G, A] CACTGCCGCCCCCTTGGCAGCTGCTCTGGGAATCGGAGCAGAGGCTGGTGTCTGGGA GCCTGGGACCTGTGCTCTCACGCTGCCCTGCTCTCAGATCTGGTAAGTCCATGC TGAGGAAGCGTTCTTGGAACCCGTTGAGCCCCAAGCACGGAGGGAGAGCGATCCA TGTCTGCTCCAGGAAACCTACTGGTGTAAAGTACTGGTGGCCAGGGACTGCCGGCACTC CCTGGAGTTGGTGGGAGGTCTGAGGCCATCCCTCCACTCTCACTGTCGTTGGGCAA
22757	CGGCGGCCCGGAAGGCCGGAGGATGGCACAGCATCCCTCATGGCATTTGCTGCCGTAGCG AGAAGGTATCTCTAATGGACTCCACTTCCAGCCCTGGCCCTCCCCACTCTTCAGCCT GGCCTTGCGGACCCCTCATGGCTGGTCCCGGCCCCCTCCTCATGTAACAGTGGCATCCG GCTCCTCACCAATTCCAGGAATATGCCCGCAGCTGCCAGCGCCCGTGTCTTGCCCTGC CATTTATGCTGTGCTGATTGAGATGGGACCCGACTGCCGCCCCCTGGCAGCTGCTCT [C, T] GGGAATCGGAGCAGAGGCTGGTGTCTGGAGCCTGGACCTGTGCTCTCACGCTGCC TTGTCTCTCAGATCTGGTGAAGTCCATGCTGAGGAAGCGTCTCTGGGAACCCGTT TGAGCCCCAAGCACGGAGGGAGAGCGATCCATGCTGCTCCAGAAACCTACTGGTGT AGTACTGGTGGGCCAGGGACTGCCGGCACTCCCTGGAGTTGGTGGGGAGGTCTGAGGC CCATCCTCCACTCTCACTGTCGTTGGCCAAGGCCAGGCCTGGGACTTGGCCAGGTC
22779	ATGGCACAGCATCCCTCATGGCATTTGCTGCCGTAGCGAGAAGGTATCTCTAATGGACT CCCACCTCCAGCCCTGGCCCTCCCCACTCTTCAGCCTGCCCTGCCGACCCCTCATGGG CTGGTCCCGGCCCTCCTCATGTAACAGTGGCATCCGGCTCTCACCATTCAGGAATA TGCCCCCAGCTGCCAGCGCCCGTGTCTTGCCCTGCCATTATGCTGTGCTGATTGA GATGGGACCCGACTGCCGCCCCCTGGCAGCTGCTCTCGGGGAATCGGAGCAGAGGCTG [C, T] GTGTCTGGGAGCCTGGACCTGTGCTCTCACGCTGCCCTGCTCTCAGATCTGGT AACTCCATGCTGAGGAAGCGTCTCTGGGAACCCGTTGAGCCCCAAGCACGGAGGGAA GAGCGATCCATGCTGCTCCAGAAACCTACTGGTGTAAAGTACTGGTGGCCAGGGACTG CCGGGCACTCCCTGGAGTTGGTGGGAGGTCTGAGGCCATCCCTCACTCTCACTGTC GTTGGCCAAGGCCAGGCCTGGGACTTGGCAGGTCTGGTGTGGCCCATTTGCAT
24350	AGGGAGAGCCTATAATGAGGTGGGGGCTGGAGAGGCCCTGGAGGTCCCAACTGCAGC TTTCTGTCATCTCTCAGGGAGGTGGTGCCTGGTGGGGAGGATTCTCTGAGCTCATCC AGGAATGTAGGCCCTGATGCTGGAAATTGTGCTTAGTGTAGGGGGAGAGGGGCAATAT AATTGACGTCAAATGGGACATTGGAGAGTGAAGGGGAAGCCATTAAATAATTATG CCAGCACGGCCGGTGCCTGCGCTCACGCCGTAACTCCAGCACTTGGGAGGCCAGGC [T, G] GGTGGATCACAGGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTC

FIGURE 3Q

TACTAAAAATACAAAAAAATCAGCTGGCGTGGTGGCGGGCACCTGGAGTCCCAGCTACTC
 AGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCAGAGCTTCAGTGAGCCAAGG
 TCACGCCACTGCACTCCAGCCTGGCGACAGAGTGAGACTCCGTCTAAAAAATAAT
 TATTATGCCAGCATGGTGGCTCATGCCATAATCCCAGCACTTTGGGAGGCCAGGCAGG

 24558 GAGAGTGAAGGGGAAGCCATTAATAATTATGCCAGCACGGCGGGTGCAGTCAGG
 CCTGTAATCCCAGCACTTGGGAGGCCAGGCTGGTGGATCACAGGTCAGGAGATCGAG
 ACCATCCTGGTAAACACGGTAAACCCCGTCTACTAAAAAATACAAAAAATCAGCTGG
 CGTGGTGGCGGGCACCTGGAGTCCCAGCTACTCAGGAGGCTGAGGCCAGGAGAATGGCG
 AACCCGGGAGGCAGAGCTGCAGTGAGCCAAGGTCAAGCCACTGCACTCCAGCCTGGCG
 [T, C, A]
 CAGAGTGGAGACTCCGCTCTAAAAAATAATTATGCCAGCATGGTGGCTCATGCC
 ATAATCCCAGCACTTGGGAGGCCAGGCTTGAGGCCAGGAGTTCAAGACCA
 GCCTGGGCAACATAGCAAGACCCCATCTCTAAAAAAAATTAGCCGGCGTGGT
 GTGGGTGCGTAGTCCCAGCAACTCAGGAGGCTGAGGTGGGAGGATTGCTTGAGTCTGG
 GAGGTGGAGGTTGCAGTGAGCTGAGATTGCCACTGTACTCCAGCCTGGGTGACAGAGC

 24872 CAAGACCCCACCTCTAAAAAAAATTAGCCGGCGTGGTGGTGGTGCCTGTAGT
 CCCAGCACTCAGGAGGCTGAGGTGGGAGGATTGCTTGAGTCTGGGAGGTGGAGGTTGCA
 GTGAGCTGAGATTGCCACTGTACTCCAGCCTGGGTGACAGAGCCAGACCCCTGTCTC
 [-, A]
 AAAAAGAAAAAGAAAAAGTAATAATAATTATGCCAGGACAGCAGGTGGACGGACACC
 TGGTCCTCTGACTCAGAGCCTGTGGTCCAGCACCCCCCTAGTGGTGAACAAGCCAGACA
 CAGGATAAGGATACATTAGTGTCTAGTTGTACCTGGCAAACAGAGTGACAAGATTGGG
 CTTAATACTTCCAGCTATAAAATTCTAGAATTCTGTGACCCAAGTTAATTGGGTAG
 AGCTTTTAAAAAAAATAGAGATGGAGTCTTGCCATGTTGCCAGGCTGGACTTAAAC

 25756 AGCTGGGATTACAGGTGCATGCCACCACACCCGGCTAATTGGTATTGGTATTAGAG
 ACGGGATTTCACCATTTGGCCAGGCTGGTCTAAACTCCTGACCTCAGGTAACTGCC
 ACCTCAGCCTCCAAAGTGTGGGATTACAGGCGTGAGCCACTGTGCCGGCATAGAGT
 TTTTATACTTGGATAATTGTAGAAACTCAGTAGTAGAGTTAAGTGGAGTTGGCCTT
 TTAAAGATATCAAACCCATTACTGGTATTAAAAGAGACATTGGGAGGAAA
 [C, T]
 TAGATATAGAAATCTGTTGAATATGTGACAGAACCCAGACTGATAGATGGACTCTGCC
 CTGTGAACAAGGAAAGAAAAATGAAAATGAAAGCCTCTACCCAGATCTGCTGGGG
 ATGACTGAGGTCAACACAGAAGGCCCTCAGGCCGGCACGGTGGCTACGCCGCAATCC
 CAACACTTAGGAGGCTGAGGTGGATGGATCGCTTGAGGCCAGGAGTTGAGACCAGCCT
 GGGCAACATGGTAAACCCCTGTTTATAGAGATAAAAATACAAAATTAGCTGGCG

 25968 GTAGTAGAGTTAAGTGGAGTTGGCTTTAAAGATATCAAACCCATTACTGGTTAT
 TTTAAAAGAGACATTGGGAGGAAAATAGATATAGAAATCTGTTGAATATGTGACAG
 AATCCCAAGACTGATAGATGGACTCTGCCCTGTGAACAAGGAAAGAAAAATGAAAATG
 AAAGCCTCTACCCAGATCTGCTGGGGGATGACTGAGGTCAACACAGAAGGCCCTCAGG
 CCGGGCACGGTGGCTCACGCCCTGAATCCAAACACTTAAAGGAGGCTGAGGTGGATGGATC
 [G, A]
 CTTGAGGCCAGGAGTTGAGACCAGCCTGGCAACATGGTAAACCCCTGTTTATAGAG
 ATAAAAAAAATACAAAATTAGCTGGCGTGGTGGCATGTGCTGTAGTCTCAGCTACTCA
 GGAGGCTGAGGTGGGAGGATCGCTTGAGCCTGGAAGGAGAGGTTGCAATGAGCTGAGAT
 TGCAACACTGCACTGAGCCTGACGACAGAGCGAGACGCTGTCTAAACAAACAACAA
 ACCACACACAGAGAGAAGGCCCTGATTAGGCTGATAGTTGGAGGATGTAGGGAGTC

 26537 TTAGGCTGATAGTTGGAGGATGAGGGAAAGTCAGCTGGTCAGACTGTGAGGAGCCTCCAG
 AGGCCGTGCTGGGAGGTTAGACCTCATCTGGTCAATGGGGGCCACGGAGCGTTGC
 GGGCTGAGACTGGGGCTGAGAGACCCGAAGGAGCAACTGCCGTGATGTAGGGAGGCCA
 GAGGGAGGCCAAGCTTGGGAGCTGGTGAAGGGGGCTTGAAGAGATGTGGGATTGAGAT
 TCCCTGTGTGTGAGGGAGAGTGTCTCCCTGAGTCATATTCTGACCCCTGAGGTCCCTCT
 [G, C]
 TCCCTGGTGTCCCTGAACAGGAAAGAAGGGTTGGTGAAGGGGGCAAGAGCCCAGAGCT
 CCCCGGCGTCCAGGAAGACGAGGCTGCATCCTGAGCCCTGCATGCACCCAGGGCCACCC

FIGURE 3R

GGCAGCACACTCATCCCGCGCCCTCCAGAGGCCCACCCCTCATGCAACAGCCGCCCGC
AGGCAGGGGGCTGGGACTGCAGCCCCACTCCCGCCCTCCCCATCGTGTGCATGACC

28204 CCTGGAAACATGGATGGACAAGGGCTTTGGCCACAGGTGTGGGTGTCTGTGGAGGAG
GGCTTGTTGGAGAAGGGAGGCTGGCTGGGGAGAAACCCGGATCCGCTGCATCTCCGC
GCCTGTGGGTGCATGTCGCGTGCATCTGTTGACACAGCTACTCGTATGTCCGTGCAC
TGGTACATGCATCTGAATACAGTTCTACGTCTATTAAAGGCTAGGAGCCGAATGTGCC
CCATTGTCAGTGGTCCACGTTCTCCCCGGCTCTGGGCTAAGGCAGTGTGGCCCGA
[C, T, A, G]
GCTTAAAAAGTTACTCGGTACTGTTTAAGAACACTTTATAGAGTTAGTGGAAAGGCAA
GTTAAGAGCCAATCACTGATCCCCAAGTGTCTTGAGCATCTGGCTGGGGGACCACT
TTGATCGGACCCACCCCTGGAAAGCTCAGGGTAGGCCAGGTGGATGCTACCCCTGTC
ACTGAGGGTTTGGTGCATGTTGAATGTAGCACAAGCGATGAGCAAACCTCT
ATAAGAGTGTAAAATTAACCTCCAGGAAGTGAAGTTAAAACAATAAAAGCCCTT

FIGURE 3S